

Table 70: Comparative Sequences relating to SAG 1280

ATACCTTTATTGAGTTTGAAAACCTTGGAAATTGATTTCTTTTGTGGATGAGGCTCATC
 ACTTCAAGAAATATCCGTCCAATCACTGGACTTGGGAATGTAGCTGGAATCACCACACAA
 CTTCTAAAAAGAACGTTGGATATGGAGATGAAGGTGAGACAGTACAGGCAGAGCATGGAG
 ATAGAAATGTCTGTTTTCGACAGGAACACCAAGTTTCTAACTCTATTAGTGAACCTTTCA
 CCATGATGGATTACATTCAACCTGATGTCTTGGAAACGATACCTGGTATCAAAATTTGACT
 CCTGGGTTGGGGCTTTTGGGAATATCGAAAACCTCATGGAAGTACCCCGACAGGAGATA
 AGTACCAACCCAGAAACGTTCAAGAAATTTGTCAACCTTCCTGAACTCATGCGAATCT
 ACAAGGAACTGCCGATATTAGACCTCAGACATGCTTGATTACCAGTACCGGAAGCTA
 AGATTATTGCGGTGGAAAGCGAGTTAACGCAAGCTCAGAAATACTATTGGAAGAGCTGG
 TAAAGCGTTGACAGCTATCAAGTCAGGTAGTGTGATCCAAGTAGAGATAACATGCTTA
 AAATCACAGGAGAAGCCGAAACCTAGCTATTGATATGCGGTTGATTGACCTACTTACT
 CCTTATCGGATTAATCAGAAATCCTTCAAGTAGTTCGATAATGTCGAGCGGATTACCGTG
 ATGGAGCTGGAGACAAGCCACTCAGATGATTTCTCAGATATTGGAACCCCTAAAGTA
 AGGAAGAAGGGTTTGATGTCTACAATGAACCTTAAGGACTTGTTTGTGCGATCGAGGGATAC
 CAAAAGAGAAATTTGCTTCCATGATGCCAATCTGATGAGAAGAAAACTCTCTGT
 CAGCAAGGTCAATAGTGGAGAAAGTACGGATTCTCATGGCTTCTACGGAAGGAGGGGAA
 CAGGATTAACGCTCAATCTCGCATGAAAGCTGTCCACTATTAGACGTTCCCTGGAGGC
 CCTCAGACATTTGTCAGCGAAATGGACGACTAATTCGACAAGGAAACATGCACAGGAGG
 TAGATATTATCACTAATATTACTAAAGGGAGCTTTGACAATTACCTCTGGCAGACGAGG
 AGAATAAGCTAAAGTATATCACCCAGATAATGACCTCAAAGATCCTGTGAGATCAGCTG
 AAGACATTGATGAACAAACCATGACCGCTCAGACTTTAAGGCATTGGCAACTGGGAACC
 CTTATCTCAAACCTCAAATGGAGTTGGAAAATGAACCTGACAGTTTATAGAGAACTCAAAC
 GAGCCTTTAATCGCTCCAAAGACGAGTATCGCCATACCATTTCTATAGCGAGAAGCACC
 TCCTTATTATGGAAGAACGTTGAGTCAATATGATAAAGATATTGCCCAATCTTTGGCAA
 CCAAGTCGCAAGATTGTTGTCATGCGATTGACAATCAAGCAATGGATAATCGTGCTGAAG
 CTGGGGACTATCTGCGAAACCTATTACCTATAACCGCTCAGAGACCAAGGAAGTCAGGA
 CACTTGCAGCTTTAGAGGATTTGATTTAAAAATGACTACACGAGGTGCTAGTGAGCCCT
 TACCAGAAACCATTTCTTAAATGATTGATGGTATGATACAGTATCTGTCGCCCTTGATT
 TGAATATCAGACCTGGGAACCATTTCAACGATTAGTAATGCCATTGACCATATTATAGATG
 ACCAAGAAAAGACGCAAGAGCTGGTAAAGGATTTAAAGATAAGCTACAGTAGCCAAAG
 TAGAAGTTGATAAAGTCTTTCCAAAGGAAGAGGACTATCAGCTTGTAAGGCTAAGTATG
 ATGTTTATGCTCCCTTGGTTGAAAAGAGAGCAGAGATTGAAGAGATAGATGCAGCTTTGG
 CCAAGTTTAGTGAAGATACAACCCCCAAAAGCAACAAATAGCACTCGAGATA

SEQ ID. NO. 7002

STRAIN H36B

GGAGGGAAAATGAATCAAGAAGTCTTACTACAAATGAT
 GAGAGCCACTATTCCTCGTATAGAGCCCTTGCTTGAGGCATTTTATATT
 ACCAAGCAGAGCATTTTGATGAGGAGTGGGATAGTCTTATTCATCAGTTT
 ATGACCAATAGGCAAGAAATAAATAAGTCTGTTCAAGTACTTCACTTTGA
 GACAGATGTTTCAGCTTTTGTCCAGGCTAGTCTTATGATAGTCTCATG
 ATCTATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACATA
 GATAAATATCGCCGCTCGAAAAAACCTTGGTGATAGAAGTGGCCTTGT
 CAATCTGGCCACTCGTTTCAATTATTGGATTCCAATGGACACTACCAA
 CCATATCGCCGATTCACTCTTACAAAAGAGTAGGGAGCTAATTGGTC
 AATGTGTATCGTGTGGCTAATAATTAGCGGATCGTATTAGTCGAGATAT
 TGAACAGTTTCTCTAACTTACGAGCTTGAGCTTGAACCTAGAGCTGATG
 AAAGTGTCTAGAAAATGAAGAACTGTGATGAGCAGCAAAAACAGTGTT
 CATCAAGCAATATCTTTCGAGAAGAGGGCTCTCTGTTATTGCTAGTTT
 GGATGTAGATTGTTCTCAACTAGATGTTCAAAATAGGAAAAACAGTCATC
 TGCCAGCTTATGAAGAGTTATCCTTACGACGTAAATTTGAGATTCTAACA
 TATTTTGACCAAAATCGAAATGAACGTTCCAAAGTCCCAAGTTTATAGAG
 AGGTGATTTTGACACAGAGATGGAAATGACACAGTCTTTGATGGCGAGG
 AATTACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGA
 ACGCTGACTACAGTCAAGAGAAAAGGAATTAGAAAAAATTGGACAAGCCAT
 TAGGATAGAAAATCAAGAAAATGACTCAGCTA₅GkATTGrTTTATCTC
 AGTTTGACCCAGACCGAGTCGGTATTTTATTGKATGCAGCAGGTCGTYT
 CGTTTAWAWAATGCAGACCTTGCTTCACTAGGTGGTTATCCAAAGCCTC
 GGTAACTCAACTAGCCCTTGCGACAGAACTACTCCAAATGGGACTAAGTC
 ATGAAAAGGTTGAATTTTCTTTGGTAGCCAGCTTCCATGAAGAGCTG
 CGACAAGTTGCCTACGCCCTTTTACACCAAGAACTCAGCAGAGAAGATGC
 GGAGCAATTTGAAAAAGATAAAGGTAATCAGCCAGATTAACTCTCAGAG
 ATTGGAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAGTAGTTGATGAA
 GAATTCGCGGAAAATCCACTGGTTAGAGAGTATTGGACACTTATCCTCT
 GGGGTCAITGGTTTCTATAAGGGACAGGACTTTGAGGTCATGTGCGTCA
 GCGATGCTCGATGAACGGTTTGATTGCGATTGAGTTAGTCAATGACTTT
 TCGGATATCATTGAACAAAATCCAGTTCTTTATGTGAGGACCTGGGAAGA
 AGTCAGTCAGGCACTTCATCAGCCAAAGGCAGAACCAAAACAGAGTTAG
 AAGAAGCGGACCAAGAATTAAACCTATTCTCATTTCTGGAAGAGGAGCTA
 GTTCAGAGTATTGGACTATTGGAAACAGATGATTAGAAAAATGGTCATAA
 CGATACTGATCTTGAAGAAAACAGATAATCAAAATTCCTGAAGAGGAAGTCG
 TCGAAACAATTCAGAGATTCCAGTAAACGGACTTTTATTTTCAGAAAGAT
 TTGACGGACTTTTATCCTAAGACTGCTAGAGATAAGGTTGAGACAAAACAT
 TGTGGCCATTCTTTGGTAAAAATCTAGAAGTAGAGCACCAGCAATGCTT
 CACCAAGTGAACAAGAACTCCTTGCAAGTATGTAGGCTGGGGTGGACTA
 GCCAATGAATTTTGTGACTATAATCCAAATTTTCTAAGGAACGAGA
 AGAACTGAAGAGCTAGTCACAGATAAAGAGTATTGCGATATGAACAGT
 CCTCCTGACAGCCTATTACACAGACCCATCCCTGATCCGTGAGATGTGG
 GATAAGTTGGAAGAGATGGCTTTACAGGTGGCAAAATCCTAGATCCTTC
 CATGGGAACAGGGAATTTCTTTGCGGCTATGCCAAAACACTTAAGAGAAA
 AGAGTGAGTTGATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCC
 AAACACCTTCATCCCAATAGTCATATTGAATTAAGGGATTTGAGACGGT
 GGCTTTTAAACGCAATAGTTTGGATTGGTGATTCAAATGTGCCCTTTG

Table 70: Comparative Sequences relating to SAG 1280

CCAATATACGAATTGCGGATAATAGGTACGATAGGCCCTTACATGATTTCAT
 GACTACTTTGTCAAAAAGTCACTTGATTGCTTCATGATGGTGGACAAGT
 AGCGATTATCTCTTCCACAGGAACATGATAGGATAAGCGAACAGAAAACATCT
 TACAAGATATTCTGAGACAACCTGAATTTCTTGGTGGGGTTCGACTGCCT
 GACTCTGCCCTTAAGGCCATTGACAGGAACGAGTGTCAACACGGATATGTT
 ATTCTTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCCT
 TTTGAGTTCCATTCCGTATGACAAGGATAGTCGCATTTGGCTCAATCCT
 TATTTTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTGAG
 GAATTTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGA
 TTGCAAGTGTGAAACAGCTCTAAATCACGTTAAGGCCCAAGAGAGATT
 GATAGAAATGAGGTCACTTAACCCAGATGTGTTGACCAACAAGTCAA
 TGATACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTGAGTACAGTT
 TTGGTTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTTCGA
 GTCGGAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

SEQ ID. NO. 7003

STRAIN 18RS21

GnAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGA
 GCCACTATTCTCGTGATAGAGCCTTGCTTGAGGCATTTTATATTACCA
 AGCAGAGCATTGATGAGGAGTGGGATAGTCTTATTTCATCAGTTTATGA
 CCAATAGGCAAGAAAATAAATAGTCTGTTCAAGTACTTCACTTTGAGACA
 GATGTTTCAGCTTTTGTCCAGGCTAGTCTTATGATACTGCTCATGATCT
 ATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACCTAGATA
 AACTATCGCCGCTGAAAAAACTTGGTGATAGAAGTGGCCTTGTTCAT
 CTGGCCACTCGTTTCAATTATTTGGATTCCAAATGGACACTACCAACCAT
 ATCGCCGATTCACCTTACAAAAGAGTAGGGGAGCTAATTTGGTCAATG
 TGTATCGTGTGGCTAATAATTTAGCGGATCGTATTAGTCGAGATATTGAA
 CAGTTTCTCTTAACCTTACGAGCCTGAGCTTGAAACTAGAGCTGATGAAAC
 TGTCTAGAAAAATGAAGAACTGTTGATGAGCACAACAAAGTGTTCATC
 AAGCAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTTGCTAGTTTGGAT
 GTAGATTTGTCTCACTAGATGTTCAAATAGGAAAAACAGTCATCTGCC
 AGCTTATGAAGAGTTATCCTTACGAGCTAAATTTGAGATTCTAACATATT
 TTGACCAAAATCGAAATGAACGTTCCAAAGTCCCAAGTTTGTAGCAGGTT
 GATTTTGACACAGAGATGGAATGACACCAAGTCTTTGATGGCGAGGAATT
 ACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGAACGC
 TGACTACAGTcGAAGAAAAGGAATTAGAAAAAATTTGGACAAGCCATTAGG
 ATAGAAAAATCAAGAAAAATGACTCAGCTAGGGATTGATTTATCTCAGTT
 TGACCCAGACCGAGTCCGTTATTTTATTTGGATGACAGCGGTCTTTTCGTT
 TAAAAAATGACAGACCTTGCTTTACTAGGTGGTTATCCCAAAGCCTCGGTA
 ACTCAACTAGCCCTTGGCAGACAGAACTACTCCAATGGGACTAAGTCATGA
 AAAGGTTGAATTTTCTTTGGTAGCCAGCTTTCCATTGAAGAGCTGCGAC
 AAGTTGCCCTACGCCCTTTTACACCAAGAACTCAGCAGAGAAGATGCGGAG
 CAATTTGAAAAAGATAAAGGTAATCAGCCAGATTAACTCTCAGAGATTG
 GAAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAGTAGTTGATGAAGAAT
 TCGCGGAAAATCCACTGTTTCCAGAGATTTGGACACTTATCTCTGGGG
 TCATTGGTTTCTTATAAGGGACAGGACTTTGAGGTCAATGTCGGTTCAGCGA
 TGCTCGATTGAACGGTTTGATTTCGGATTGAGTTAGTCAATGACTTTTCG
 ATATCATTGAACAAAAATCCAGTTCTTATGTGAGGACCTGGGAAGAAAGTC
 AGTCAGGCACTTCATCAGCCAAAGGCAGAACCAACACAGAGTTAGAAGA
 AGCGGACCAAGAATTAAACCTATTCTCATTCTGGAAGAGGAGCCAGTTT
 AGAGTATTGGGACTATTGGAACAGATGATTGAGAAATGGTTCATAACGAT
 ACTGATCTTGAAGAAACAGATAAATCAAATTCCTGAAGAGGAGTCTGCGA
 AACAAATCCAGAGATTCCAGTAACGGACTTTTATTTTCCAGAAGATTGA
 CGGACTTTTATCTTAAGACTGCTAGAGATAAGGTTGAGACAAACATTGTG
 GCCATTCTGTTGGTAAAAAATCTAGAAGTAGAGCACCAGCAATGCTTCACC
 AAGTGAAACAGAACTCCTTGCCAAGTATGTAGGCTGGGGTGGACTAGCCA
 ATGAAATTTTGTGATGACTATAATCCAAAATTTTCTAAGGAACGAGAAGAA
 CTGAAGAGCCTAGTCAAGATAAAGAGTATTCCGATATGAACAGTCCCTC
 CCTGACAGCCTATTACACAGACCCATCCCTGATCCGTGAGATGTGGGATA
 AGTTGGAAGAGATGGCTTTACAGGTGGCAAAATCCTAGATCCTTCCATG
 GGAACAGGGAATTTCTTGGCGCTATGCCAAAACACTTAAGAGAAAAGAG
 TGAGTTGTATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCCAAAC
 ACCCTCATCCCAATAGTCATATTGAAATTAAGGGATTGAGACGGTGGCT
 TTTAACGACAATAGTTTGAATTTGGTGATTTCAAATGTGCCCTTTTGCCAA
 TATACGAATTGCGGATAATAGGTACGATAGGCCCTTACATGATTTCATGACT
 ACTTTGTCAAAAAGTCACTTGATTGCTTTCATGATGGTGGACAAGTAGCG
 ATTATCTCTTCCACAGGAACCTATGGATAAGCGAACAGAAAACATCTTACA
 AGATATTCTGAGACAACCTGAATTTCTTGGTGGGGTTCGACTGCCCTGACT
 CTGCCCTTAAGGCCATTGACAGGAACGAGTGTCAACACGGATATGTTATT
 TTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCCTTTTC
 AGGTTCCATTTCGCTATGACAAGGATAGTCGCATTTGGCTCAATCTTATT
 TTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTGAGGAAT
 TTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGATGTC
 AAGTGTGAAACAGCTCTAAATCACGTTAAGGCCCAAGAGAGATTGATA
 GAAATGAGGTCACTTAACCCAGATGTGTTGACCAACAAGTCAATGAT
 ACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTGAGTACAGTTTGG
 TTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTTCGAGTGC
 GAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa31161.2{*} June 20, 2002 10:41 ..

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	GgAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
msa31161.2{327d_18RS21}	GnAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
msa31161.2{327dNT_H36B}	GgAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
Consensus	*-*****	*****	*****	*****	*****
	51				100
msa31161.2{327dNt_2603}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
msa31161.2{327d_18RS21}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
msa31161.2{327dNT_H36B}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
Consensus	*****	*****	*****	*****	*****
	101				150
msa31161.2{327dNt_2603}	ATTTTGATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
msa31161.2{327d_18RS21}	ATTTTGATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
msa31161.2{327dNT_H36B}	ATTTTGATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
Consensus	*****	*****	*****	*****	*****
	151				200
msa31161.2{327dNt_2603}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACITTGAGA	CAGATGTTTC
msa31161.2{327d_18RS21}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACITTGAGA	CAGATGTTTC
msa31161.2{327dNT_H36B}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACITTGAGA	CAGATGTTTC
Consensus	*****	*****	*****	*****	*****
	201				250
msa31161.2{327dNt_2603}	AGCITTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
msa31161.2{327d_18RS21}	AGCITTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
msa31161.2{327dNT_H36B}	AGCITTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
Consensus	*****	*****	*****	*****	*****
	251				300
msa31161.2{327dNt_2603}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAACTAGA	TAAACTATCG
msa31161.2{327d_18RS21}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAACTAGA	TAAACTATCG
msa31161.2{327dNT_H36B}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAACTAGA	TAAACTATCG
Consensus	*****	*****	*****	*****	*****
	301				350
msa31161.2{327dNt_2603}	CCGTCTGAAA	AAAACITGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
msa31161.2{327d_18RS21}	CCGTCTGAAA	AAAACITGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
msa31161.2{327dNT_H36B}	CCGTCTGAAA	AAAACITGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
Consensus	*****	*****	*****	*****	*****
	351				400
msa31161.2{327dNt_2603}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
msa31161.2{327d_18RS21}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
msa31161.2{327dNT_H36B}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
Consensus	*****	*****	*****	*****	*****
	401				450
msa31161.2{327dNt_2603}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTGGGTCAA	TGTGTATCGT
msa31161.2{327d_18RS21}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTGGGTCAA	TGTGTATCGT
msa31161.2{327dNT_H36B}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTGGGTCAA	TGTGTATCGT
Consensus	*****	*****	*****	*****	*****
	451				500
msa31161.2{327dNt_2603}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
msa31161.2{327d_18RS21}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
msa31161.2{327dNT_H36B}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
Consensus	*****	*****	*****	*****	*****
	501				550
msa31161.2{327dNt_2603}	CTTAACCTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
msa31161.2{327d_18RS21}	CTTAACCTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
msa31161.2{327dNT_H36B}	CTTAACCTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
Consensus	*****	*****	*****	*****	*****
	551				600
msa31161.2{327dNt_2603}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTC	TCAAGCAATA
msa31161.2{327d_18RS21}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTC	TCAAGCAATA
msa31161.2{327dNT_H36B}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTC	TCAAGCAATA
Consensus	*****	*****	*****	*****	*****
	601				650
msa31161.2{327dNt_2603}	TCITTTTCGAG	AAGAGGGCTC	TCITGGTTATT	GCTAGTTTGG	ATGTAGATT
msa31161.2{327d_18RS21}	TCITTTTCGAG	AAGAGGGCTC	TCITGGTTATT	GCTAGTTTGG	ATGTAGATT
msa31161.2{327dNT_H36B}	TCITTTTCGAG	AAGAGGGCTC	TCITGGTTATT	GCTAGTTTGG	ATGTAGATT
Consensus	*****	*****	*****	*****	*****
	651				700
msa31161.2{327dNt_2603}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
msa31161.2{327d_18RS21}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
msa31161.2{327dNT_H36B}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
Consensus	*****	*****	*****	*****	*****

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	701				750
	AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
	AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
	msa31161.2{327d_18RS21}	AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA
msa31161.2{327dNt_H36B}	751				800
	ATTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
	ATTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
	msa31161.2{327d_18RS21}	ATTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG
msa31161.2{327dNt_H36B}	801				850
	CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
	CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
	msa31161.2{327d_18RS21}	CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA
msa31161.2{327dNt_H36B}	851				900
	ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
	ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
	msa31161.2{327dNt_H36B}	ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC
msa31161.2{327dNt_2603}	901				950
	GTGGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
	GTGGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
	msa31161.2{327d_18RS21}	GTGGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA
msa31161.2{327dNt_H36B}	951				1000
	TCAAGAAAAA	TTGACTCAGC	TAAGGATTGa	TTTATCTCAG	TTTGACCCAG
	TCAAGAAAAA	TTGACTCAGC	TAAGGATTGa	TTTATCTCAG	TTTGACCCAG
	msa31161.2{327d_18RS21}	TCAAGAAAAA	TTGACTCAGC	TAAGGATTGr	TTTATCTCAG
msa31161.2{327dNt_H36B}	1001				1050
	ACCGAGTCGG	TATTTTATTG	gATGCAGCAG	GTGCTtTCG	TTTAaAaAAT
	ACCGAGTCGG	TATTTTATTG	gATGCAGCAG	GTGCTtTCG	TTTAaAaAAT
	msa31161.2{327dNt_H36B}	ACCGAGTCGG	TATTTTATTG	kATGCAGCAG	GTGCTyyTCG
msa31161.2{327dNt_2603}	1051				1100
	GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACCTCACT
	GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACCTCACT
	msa31161.2{327d_18RS21}	GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG
msa31161.2{327dNt_H36B}	1101				1150
	AGCCCTTGCG	ACAGAACTAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
	AGCCCTTGCG	ACAGAACTAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
	msa31161.2{327d_18RS21}	AGCCCTTGCG	ACAGAACTAC	TCCAAATGGG	ACTAAGTCAT
msa31161.2{327dNt_H36B}	1151				1200
	AAATTTTCTT	TGGTAGCCAG	CTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
	AAATTTTCTT	TGGTAGCCAG	CTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
	msa31161.2{327d_18RS21}	AAATTTTCTT	TGGTAGCCAG	CTTCCATTG	AAGAGCTGCG
msa31161.2{327dNt_H36B}	1201				1250
	TACGCCTTTT	TatACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
	TACGCCTTTT	TatACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
	msa31161.2{327d_18RS21}	TACGCCTTTT	TatACCAAGA	ACTCAGCAGA	GAAGATGCGG
msa31161.2{327dNt_H36B}	1251				1300
	AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
	AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
	msa31161.2{327d_18RS21}	AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT
msa31161.2{327dNt_H36B}	1301				1350
	AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTTCGCGAA
	AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTTCGCGAA
	msa31161.2{327d_18RS21}	AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA
msa31161.2{327dNt_H36B}	1351				1400
	AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
	AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
	msa31161.2{327d_18RS21}	AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG
msa31161.2{327dNt_H36B}	1400				
	ATTCGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT	
	ATTCGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT	
	msa31161.2{327d_18RS21}	ATTCGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1401	TTCTTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC	GATGCTCGAT	1450
					TTCTTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC	GATGCTCGAT	
					TTCTTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC	GATGCTCGAT	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1451	TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC	GGATATCATT	1500
					TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC	GGATATCATT	
					TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC	GGATATCATT	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1501	GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG	TCAGTCAGGC	1550
					GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG	TCAGTCAGGC	
					GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG	TCAGTCAGGC	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1551	ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA	GAAGCGGACC	1600
					ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA	GAAGCGGACC	
					ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA	GAAGCGGACC	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1601	AAGAAATAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT	TCAGAGTATT	1650
					AAGAAATAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT	TCAGAGTATT	
					AAGAAATAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT	TCAGAGTATT	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1651	GGACTATTGG	AACCAGATGA	TTTCAGAAAAT	GGTCATAACG	ATACTGATCT	1700
					GGACTATTGG	AACCAGATGA	TTTCAGAAAAT	GGTCATAACG	ATACTGATCT	
					GGACTATTGG	AACCAGATGA	TTTCAGAAAAT	GGTCATAACG	ATACTGATCT	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1701	TGAAGAAACA	GATAATCAAA	TTCTGGAAGA	GGAAGTCGTC	GAAACAATTC	1750
					TGAAGAAACA	GATAATCAAA	TTCTGGAAGA	GGAAGTCGTC	GAAACAATTC	
					TGAAGAAACA	GATAATCAAA	TTCTGGAAGA	GGAAGTCGTC	GAAACAATTC	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1751	CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT	GACGGACTTT	1800
					CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT	GACGGACTTT	
					CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT	GACGGACTTT	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1801	TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG	TGGCCATTTC	1850
					TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG	TGGCCATTTC	
					TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG	TGGCCATTTC	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1851	TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA	CCAAGTGAAC	1900
					TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA	CCAAGTGAAC	
					TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA	CCAAGTGAAC	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1901	AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC	CAATGAATTT	1950
					AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC	CAATGAATTT	
					AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC	CAATGAATTT	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1951	TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG	AACTGAAGAG	2000
					TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG	AACTGAAGAG	
					TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG	AACTGAAGAG	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	2001	CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC	TCCCTGACAG	2050
					CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC	TCCCTGACAG	
					CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC	TCCCTGACAG	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	2051	CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA	TAAGTTGGAA	2100
					CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA	TAAGTTGGAA	
					CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA	TAAGTTGGAA	
					*****	*****	*****	*****	*****	

Table 70: Comparative Sequences relating to SAG 1280

Consensus	*****	*****	*****	*****	*****
	2101				2150
msa31161.2{327dNt_2603}	AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
msa31161.2{327d_18RS21}	AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
msa31161.2{327dNT_H36B}	AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
Consensus	*****	*****	*****	*****	*****
	2151				2200
msa31161.2{327dNt_2603}	GAATTTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
msa31161.2{327d_18RS21}	GAATTTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
msa31161.2{327dNT_H36B}	GAATTTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
Consensus	*****	*****	*****	*****	*****
	2201				2250
msa31161.2{327dNt_2603}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
msa31161.2{327d_18RS21}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
msa31161.2{327dNT_H36B}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
Consensus	*****	*****	*****	*****	*****
	2251				2300
msa31161.2{327dNt_2603}	CCCAATAGTC	ATATTGAAAT	TAAGGGATTT	GAGACGGTGG	CTTTTAACGA
msa31161.2{327d_18RS21}	CCCAATAGTC	ATATTGAAAT	TAAGGGATTT	GAGACGGTGG	CTTTTAACGA
msa31161.2{327dNT_H36B}	CCCAATAGTC	ATATTGAAAT	TAAGGGATTT	GAGACGGTGG	CTTTTAACGA
Consensus	*****	*****	*****	*****	*****
	2301				2350
msa31161.2{327dNt_2603}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327d_18RS21}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327dNT_H36B}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
Consensus	*****	*****	*****	*****	*****
	2351				2400
msa31161.2{327dNt_2603}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
msa31161.2{327d_18RS21}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
msa31161.2{327dNT_H36B}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
Consensus	*****	*****	*****	*****	*****
	2401				2450
msa31161.2{327dNt_2603}	AAAAAGTCAC	TTGATTTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327d_18RS21}	AAAAAGTCAC	TTGATTTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327dNT_H36B}	AAAAAGTCAC	TTGATTTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
Consensus	*****	*****	*****	*****	*****
	2451				2500
msa31161.2{327dNt_2603}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
msa31161.2{327d_18RS21}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
msa31161.2{327dNT_H36B}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
Consensus	*****	*****	*****	*****	*****
	2501				2550
msa31161.2{327dNt_2603}	GTGAGACAAC	TGAATTTCTT	GGTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
msa31161.2{327d_18RS21}	GTGAGACAAC	TGAATTTCTT	GGTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
msa31161.2{327dNT_H36B}	GTGAGACAAC	TGAATTTCTT	GGTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
Consensus	*****	*****	*****	*****	*****
	2551				2600
msa31161.2{327dNt_2603}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCITCCAGAA
msa31161.2{327d_18RS21}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCITCCAGAA
msa31161.2{327dNT_H36B}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCITCCAGAA
Consensus	*****	*****	*****	*****	*****
	2601				2650
msa31161.2{327dNt_2603}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
msa31161.2{327d_18RS21}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
msa31161.2{327dNT_H36B}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
Consensus	*****	*****	*****	*****	*****
	2651				2700
msa31161.2{327dNt_2603}	TTTCGCTATGA	CAAGGATAGT	CGCATTTGGC	TCAATCCTTA	TTTTGATGGA
msa31161.2{327d_18RS21}	TTTCGCTATGA	CAAGGATAGT	CGCATTTGGC	TCAATCCTTA	TTTTGATGGA
msa31161.2{327dNT_H36B}	TTTCGCTATGA	CAAGGATAGT	CGCATTTGGC	TCAATCCTTA	TTTTGATGGA
Consensus	*****	*****	*****	*****	*****
	2701				2750
msa31161.2{327dNt_2603}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
msa31161.2{327d_18RS21}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
msa31161.2{327dNT_H36B}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
Consensus	*****	*****	*****	*****	*****
	2751				2800
msa31161.2{327dNt_2603}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG
msa31161.2{327d_18RS21}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dnt_H36B}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG
Consensus	*****	*****	*****	*****	*****
	2801				2850
msa31161.2{327dnt_2603}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG
msa31161.2{327d_18RS21}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG
msa31161.2{327dnt_H36B}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG
Consensus	*****	*****	*****	*****	*****
	2851				2900
msa31161.2{327dnt_2603}	GTCATCATT	ACCCAGATGT	GTGACCAAA	CAAGTCAATG	ATACCTCCAT
msa31161.2{327d_18RS21}	GTCATCATT	ACCCAGATGT	GTGACCAAA	CAAGTCAATG	ATACCTCCAT
msa31161.2{327dnt_H36B}	GTCATCATT	ACCCAGATGT	GTGACCAAA	CAAGTCAATG	ATACCTCCAT
Consensus	*****	*****	*****	*****	*****
	2901				2950
msa31161.2{327dnt_2603}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG
msa31161.2{327d_18RS21}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG
msa31161.2{327dnt_H36B}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG
Consensus	*****	*****	*****	*****	*****
	2951				3000
msa31161.2{327dnt_2603}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTTCGAGT	CGGAACCAAG
msa31161.2{327d_18RS21}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTTCGAGT	CGGAACCAAG
msa31161.2{327dnt_H36B}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTTCGAGT	CGGAACCAAG
Consensus	*****	*****	*****	*****	*****
	3001				3033
msa31161.2{327dnt_2603}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	
msa31161.2{327d_18RS21}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	
msa31161.2{327dnt_H36B}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	
Consensus	*****	*****	*****	***	

SEQ ID. NO. 7004

STRAIN H36B frame: 1

GGKMNQEVLLQMMRATIPDRALLEAFLLYQAEHFDEWDLSLIHQFMTNRQEIINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSTVHQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHPAYEELSRLR
KFEILTTFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAIRIENQEKLTQLXIXLSQFDPDRVGILLXAGRXRLKNADLASLGGYP
KASVTQLALATELLQMGSLSEKVEFFFGSLSIEELRQVAYAFHQLSREDAEQFEKDK
GNQPDLTLRDWSKLEKAEKVEVDEEFAENPLVQVRVLDTPGLSLVSYKGQDFEVM SVS
DARLNGLRIRIELVNDFSDI IEQNPVLYVRTWEEVSQALHQPKAEPQTELEADQELNLS
FLEELVQSIGLLEPDDSENGHNDTLEETDNQIPBEEVETIPEIPVTDYFYPEDLTDF
YPKTARDKVETNI VAI RLKVNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPMTGTGNFF
AAMPKHLREKSELYGVELDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVI SNVPFA
NIRIADNRYDRPYMIHDYFVKKSLDLLHDGGQVAI ISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLKGYVADDLAFSGSIRYDKDSRIWLNPFYFDG
EYNSQVLGTYEVRNFGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVI INPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYVYRDNGKIRVGTKTEEISYYVDEE

SEQ ID. NO. 7005

STRAIN 18RS21 frame: 1

GGKMNQEVLLQMMRATIPDRALLEAFLLYQAEHFDEWDLSLIHQFMTNRQEIINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSTVHQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHPAYEELSRLR
KFEILTTFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAIRIENQEKLTQLGIDLSQFDPDRVGILLDAAGFRRLKNADLALLGGYP
KASVTQLALATELLQMGSLSEKVEFFFGSLSIEELRQVAYAFHQLSREDAEQFEKDK
GNQPDLTLRDWSKLEKAEKVEVDEEFAENPLVQVRVLDTPGLSLVSYKGQDFEVM SVS
DARLNGLRIRIELVNDFSDI IEQNPVLYVRTWEEVSQALHQPKAEPQTELEADQELNLS
FLEELVQSIGLLEPDDSENGHNDTLEETDNQIPBEEVETIPEIPVTDYFYPEDLTDF
YPKTARDKVETNI VAI RLKVNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPMTGTGNFF
AAMPKHLREKSELYGVELDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVI SNVPFA
NIRIADNRYDRPYMIHDYFVKKSLDLLHDGGQVAI ISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLKGYVADDLAFSGSIRYDKDSRIWLNPFYFDG
EYNSQVLGTYEVRNFGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVI INPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYVYRDNGKIRVGTKTEEISYYVDEE

SEQ ID. NO. 7006

STRAIN 2603 frame: 1

GGKMNQEVLLQMMRATIPDRALLEAFLLYQAEHFDEWDLSLIHQFMTNRQEIINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSTVHQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHPAYEELSRLR
KFEILTTFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAIRIENQEKLTQLGIDLSQFDPDRVGILLDAAGFRRLKNADLALLGGYP
KASVTQLALATELLQMGSLSEKVEFFFGSLSIEELRQVAYAFHQLSREDAEQFEKDK
GNQPDLTLRDWSKLEKAEKVEVDEEFAENPLVQVRVLDTPGLSLVSYKGQDFEVM SVS

Table 70: Comparative Sequences relating to SAG 1280

DARLNGLIRIELVNDFSDIIEQNPLYVVRTWEEVSQALHQPKEPQTELEBDAQELNLFSS
 FLEEEPVQSIGLLEPDDSENGHNDTDLEETDNQIPEEEVETIPEIPVTDFFYPEDLTDF
 YPKTARDKVTENIVAIRLVNLEVEHRNASEQELLAKYVGWGLANEFFDDYNPKFSK
 EREELKSLVTDKEYSDMKQSSLTAYTTPSLIRQMWDLKLERDGTGGKILDPGSMGTGNFF
 AAMPKHLREKSELYGVELDTITGAIAKHLHPNSHIEIKGFETVAFNDSFDLVI SNVPPA
 NIRIADNRYDRPYMIHDYFVKSLDLLHDGGQVAIISSTGTMDKRTENILQDIRETTEFL
 GGVRLPDSAFKAIAGTSVTMDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPFYDG
 EYNSQVLGTYEVRNFGGTLGKGTSDDLIASVETALNHVKAPREIDRNEVINPDLVTK
 QVNDTSIPAEEMRENLGQYSGYQGSTVYVRDNGKIRVGTKTEEISYYVDEE

PRETTY of: /biotmp/msa23816.2{*} June 20, 2002 11:04 ..

msa23816.2{327dNT_H36B}	1	50
msa23816.2{327dNT_2603}	gGKMNQEVLL QMMRATIPRD RALLEAFLLY QAEHFDEEWD SLIHQFMTNR	
msa23816.2{327d_18RS21}	gGKMNQEVLL QMMRATIPRD RALLEAFLLY QAEHFDEEWD SLIHQFMTNR	
Consensus	-***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	51	100
msa23816.2{327dNT_2603}	QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS	
msa23816.2{327d_18RS21}	QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	101	150
msa23816.2{327dNT_2603}	PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RANLVNVYR	
msa23816.2{327d_18RS21}	PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RANLVNVYR	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	151	200
msa23816.2{327dNT_2603}	VANNLADRIS RDIEQFLITY EPELETRADE TVLENEETVD EHKTSVHQAI	
msa23816.2{327d_18RS21}	VANNLADRIS RDIEQFLITY EPELETRADE TVLENEETVD EHKTSVHQAI	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	201	250
msa23816.2{327dNT_2603}	SFREGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ	
msa23816.2{327d_18RS21}	SFREGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	251	300
msa23816.2{327dNT_2603}	IRNERSKVPS FRRGDFDTEM EMTPVFDGEE LLTYLEADGS PYELKRTLIT	
msa23816.2{327d_18RS21}	IRNERSKVPS FRRGDFDTEM EMTPVFDGEE LLTYLEADGS PYELKRTLIT	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	301	350
msa23816.2{327dNT_2603}	VEEKELEKIG QAIRIENQEK LTQLxIxLSQ FDPDRVIGILL xAAGRrRLxN	
msa23816.2{327d_18RS21}	VEEKELEKIG QAIRIENQEK LTQLgIdLSQ FDPDRVIGILL dAAGRfRLkN	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	351	400
msa23816.2{327dNT_2603}	ADLAsLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA	
msa23816.2{327d_18RS21}	ADLAlLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA	
Consensus	****-***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	401	450
msa23816.2{327dNT_2603}	YAFhQELSR EDAAQFEKDK GNQPDLTlRD WSKLEKAEG KEVVDEEFAB	
msa23816.2{327d_18RS21}	YAFlyQELSR EDAAQFEKDK GNQPDLTlRD WSKLEKAEG KEVVDEEFAB	
Consensus	****-***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	451	500
msa23816.2{327dNT_2603}	NPLVQRVLDL YPLGSLVSYK QGDFEVMSVS DARLNGLIRI ELVNDFSDI	
msa23816.2{327d_18RS21}	NPLVQRVLDL YPLGSLVSYK QGDFEVMSVS DARLNGLIRI ELVNDFSDI	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	501	550
msa23816.2{327dNT_2603}	EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFSS FLEEEpVQSI	
msa23816.2{327d_18RS21}	EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFSS FLEEEpVQSI	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	551	600
msa23816.2{327dNT_2603}	GLLEPDDSEN GHNDTDLEET DNQIPEEEV ETIPEIPVTD FYFPEDLTDF	
msa23816.2{327d_18RS21}	GLLEPDDSEN GHNDTDLEET DNQIPEEEV ETIPEIPVTD FYFPEDLTDF	
Consensus	***** ***** ***** ***** *****	

Table 70: Comparative Sequences relating to SAG 1280

	601				650
msa23816.2{327dNT_H36B}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
msa23816.2{327dNT_2603}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
msa23816.2{327d_18RS21}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
Consensus	*****	*****	*****	*****	*****
	651				700
msa23816.2{327dNT_H36B}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
msa23816.2{327dNT_2603}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
msa23816.2{327d_18RS21}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
Consensus	*****	*****	*****	*****	*****
	701				750
msa23816.2{327dNT_H36B}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
msa23816.2{327dNT_2603}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
msa23816.2{327d_18RS21}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
Consensus	*****	*****	*****	*****	*****
	751				800
msa23816.2{327dNT_H36B}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
msa23816.2{327dNT_2603}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
msa23816.2{327d_18RS21}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
Consensus	*****	*****	*****	*****	*****
	801				850
msa23816.2{327dNT_H36B}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
msa23816.2{327dNT_2603}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
msa23816.2{327d_18RS21}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
Consensus	*****	*****	*****	*****	*****
	851				900
msa23816.2{327dNT_H36B}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPYFDG
msa23816.2{327dNT_2603}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPYFDG
msa23816.2{327d_18RS21}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPYFDG
Consensus	*****	*****	*****	*****	*****
	901				950
msa23816.2{327dNT_H36B}	EYNSQVLGTY	EVRFNNGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
msa23816.2{327dNT_2603}	EYNSQVLGTY	EVRFNNGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
msa23816.2{327d_18RS21}	EYNSQVLGTY	EVRFNNGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
Consensus	*****	*****	*****	*****	*****
	951				1000
msa23816.2{327dNT_H36B}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTK
msa23816.2{327dNT_2603}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTK
msa23816.2{327d_18RS21}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTK
Consensus	*****	*****	*****	*****	*****
	1001	1011			
msa23816.2{327dNT_H36B}	TEEISYYVDE	E			
msa23816.2{327dNT_2603}	TEEISYYVDE	E			
msa23816.2{327d_18RS21}	TEEISYYVDE	E			
Consensus	*****	*			

Table 71: Comparative Sequences relating to SAG1333

SEQ ID NO. 7101

STRAIN 2603

ATGAAAAAGAAAATTTATTTGAAAAGTAGTGTCTTGGTTTAGTCGCTGGGACTTCTATT
 ATGTTCTCAAGCGTGTTCGCGGACCAAGTCCGGTGTCCAAGTTATAGGCGTCAATGACTTT
 CATGGTGCACCTTGACAATCTGGAACAGCAAATATGCCTGATGGAAGTTGCTAATGCT
 GGTACTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAACAACT
 AACCCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGTTGGAGCAAGTCCAGCC
 AACTCTGGGCTTCTTCAAGATGAACCAACTGTCAAAAATTTAATGCAATGAATGTTGAG
 TATGGCACATTGGGTAACCATGAATTTGATGAAGGGTTGGCAGAATATAATCGTATCGTT
 ACTGGTAAAGCCCCGTCTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACAT
 GAAGCTGCAAAACAAAGAAATTTAGTAGGCAAAATGTTATGATAAAGTTAACAACAAAT
 CCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCCTGTAATAACAAAAGTGTGAAC
 GTTGGCTTTATCGGGATTGTACCAAGACATCCCAACCTTGTCTTACGTAAAAATTA
 GAACAATATGAATTTTAGATGAAGCTGAAACAATCGTTAAATACGCCAAGAAATTACAA
 GCTAAAAATGTCAAAGCTATTGTAGTTCTCGCACATGTACCTGCAACAAGTAAAAATGAT
 ATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTGAAAAAT
 AGCGTAGATATTGTCTTGTCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAA
 ACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGTCTTA
 GATACTGATACACAAGATTCTTATTGAGACCCCTTCAAGCTAAAGTAATTGCAGTTGCTCCT
 GGTAAAAAAGCAGGTAGTCCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTT
 AAACAAGTAAACAGAAAGCAAAAATTTGGTACTGCCAGGTAAAGTGTATGATTACGCGTTCT
 GTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCAGAGGCTCACTAGCAATT
 GCTCGAAAAAGCTGGCCAGATATCGATTTTGGCATGACAATAATGGTGGCAATTCTGTCT
 GACTTACTCATCAAAACAGATGGAACAATCACTGGGGAGCTGCACAAGCAGTTCAACCT
 TTTGGTAAATATCTTACAAGTCGTGCAAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAAC
 GAACAATACGACCAAAACAAAATTTCTTCTTCAATAGCTGGTCTGCGATACACTTAC
 ACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAAGCTTATAAATCA
 AATGGTGAGGAAATCAATCTGATGCAAAATACAAATTAGTTATCAATGACTTTTATTTC
 GGTGGTGGTGTGGCTTTTGGCAAGCTTCAGAAATGCCAACTTTAGAGGCAATTAACCCC
 GATACAGAGGTATTATGGCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGC
 GTTCCAATAATAAACCTTAAATCTATGTCACTATGAAGATGGTTAATGAACTATTACA
 CAAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGATCGACAAGGAAATATT
 GTAGCACAAGAGATTGTATCAGACACTTTAAACCAACAAAATCAAAATCTACAAAATC
 AACCCCTGAATCTACAAATTCACAAAAACAAATTACACCAATTTACAGCTATTAAACCTATG
 AGAAATTTATGGCAACCATCAAACTCCACTACTGTAAATCAAAACAATTACCAAAAAACA
 AACTCTGAATATGGACAATCAATCCTTATGTCTGTCTTGGTGTGGACTTATAGGAATT
 GCTTTAAATCAAAAGAAAAACATATGAAA

SEQ ID NO. 7102

STRAIN 090

AAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGAC
 AATACTGGAACAGCAAAATATGCCTGACGGAAGTTACTAATGCTGGCAC
 TGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAAC
 AAATAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGGTT
 GGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTAA
 AACATTTAATGCAATGAATGTTGAGTATGGCATTAGGTAACCATGAAT
 TTGATGAAGGTTTGGCAGAATAAATCGTATCGTTACTGGAAAGGCCCT
 GCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAGC
 TGCAAAACAGAAATTTAGTAGGCAAAAGTTATTGATAAAGTTAACAAC
 AATCCCTTACAATTTGAAACCTTACGCTATTAAAAATATCTCTGTAAT
 AACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATCCC
 AAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTATAGTGAAG
 CTGAAACAATCGTTAATACGCCAAGAAATTACAAGCTAAAAATGTCAAG
 GCTATTGTAGTCTTGTCTCATGTACCTGCAACCAAGCAAGGATGATATTGC
 TGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTG
 AAAATAGCTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAAT
 GGTCTTGTGGTAAAACTCGCATTGTACAAGCGCTCTCTCAAGGAAAAGC
 CTATGCTGACGTACGTGGTGTCTTATAGTACTGATACACAAGATTTCATTG
 AAACCCCTTCACTAAAGTAGTTGAGTGTCTCTGGTAAAAAAGCAGGT
 AGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACA
 AGTAACAGAAGCTAAATTTGTTACTGCCGAGGTAAGTGGCATGATTACGC
 GTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCAGCCTCATCAGAG
 GCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGGCCAT
 GACAAATAATGGTGGCATTCTGTCTGACTACTCATCAACCAAGATGGAA
 CAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTA
 CAAGTCGTGGAATTTACTGGTAGAGATCTTTATAAAGCACTCAACGAACA
 ATACGACCAAAACAAAATTTCTTCTTCAAAATAGCTGGTCTGCGATACA
 CTTACACAGATAATAAAGAGGGCGGAGAAGAAACACCATTTAAAGTTGTA
 AAAGCTTATAAATCAAAATGGTGAAGAAATCAATCCTGATGCAAAATACAA
 ATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAGCT
 TCAGAAATGCCAAACTCTAGGAGCCATTAAATCCCGATACAGAGGTATT
 ATGGCTTATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCC
 AAATAATAAACCTTAAATCTATGTCACTATGAAGATGGTTAATGAACTA
 TTACACAAAATGATGGTACACATAGCATTATTAAGAACTTTATTAGAT
 CGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACCA
 AACAAAATCAAAATCTACAAAATCAACCTGTAACTACAATTCAAAAA
 AACAAATTACCAATTTACAGCTATTAAACCTATGAGAAATTATGGCAAA
 CCATCAAACTCCACTACTGTAAATCAAAACA

SEQ ID NO. 7103

STRAIN A909

GCGTCAATGACTTTTCATGGTGCATTGACAATACTGGAACAGCAAAATATG
 CCTGACGGAAGTTACTAATGCTGGCACTGCTGCTCAATTAGATGCTTA

Table 71: Comparative Sequences relating to SAG1333

TATGGATGATGCTCAAAAAGATTTCAAACAACTAACCTTAATGGTGAAA
GCATTAGAGTTCAAGCTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCA
GGGCTTCTTCAAGATGAACCAACCGTTAAACATTTAATGCAATGAATGT
TGAGTATGGCACATTAGGTAAACCATGAATTTGATGAAGGTTTGGCAGAAT
ACAATCGTATCGTTACTGGAAGGGCCCTGCTCCaGaTTCTAATATAAAT
AATATTACGAAATCATACCCACAGAGCTGCAAAACAAGAAATTTAGT
GGCAACGTTATTGATAAAGTTAAACAAACAAATCCCTTACAATTGGAAAC
CTTACACTATTAAAAATATTCTGTAAATAACAAAAGTGTGAACGTTGGC
TTTATCGGAATCGTTACCAAGACATCCCAACCTTGTCTTACGTAAAAA
TTATGAACAATATGAATTTTATAGATGAAGCTGAAACAAATCGTTAAATACG
CCAAAGAATTACAAGCTAAAAATGTCAAGGCTATTGTAGTCCTTGCTCAT
GTACCTGCAACAAGCAAGGATGATATTGCTGAAGGTGAAGCAGCAGAAAT
GATGAAAAAAGTCAATCAACTCTTCCCTGAAAAATAGCGTAGATATTGTCT
TTGCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAAACTCGT
ATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGCTGATGTCGTGGTGT
CCTAGATACTGATACACAAGATTTCAATTGAAACCCCTTCAGCTAAAGTAA
TTGCAAGTTGCTCCTGGTAAAAAAGAGGTAGTGGCGATATTCAAGCCATT
GTTGACCAAGCTAATACTATCGTTAAACAGTAACAGAAGCTAAAAATGG
TACTGCCAGGTAAAGTGGCATGATTACGCGTTCTGTTGATCAAGATAATG
TTAGTCCGGTAGGCAGCTCATCACAGAGGCTCAACTAGCAATTGCTCGA
AAAAGCTGGCCAGATATCGATTTTGCCATGACAAATAATGGTGGCATTCG
TGCTGACTTACTCATCAACAGATGGAACAAATCACCTGGGGAGCTGCAC
AAGCAGTTCAACCTTTTGGTAATATCTTACAAGTCTCGAAATTACTGGT
AGAGATCTTTATAAGCACTCAACGAACAATACGACCAAAAAACAAATTT
CTTCTTCAAATAGCTGGTCTGCGATACACTTACACAGATAATAAGAGG
GCGGGGAAGAAACACCAATTTAAAGTTGTAAGAGCTTATAAATCAAATGGT
GAGGAAATCAATCCTGATGCAAAATACAAATAGTTATCAATGACTTTT
ATTGGTGGTGGTGGTGGCTTTGCAAGCTTCAGAAATGCCAACTTCTAG
GAGCCATTAAATCCGATACAGAGGTATTTATGGCCTATATCACTGATTTA
GAAAAAGCTGGTAAAAAAGTGAAGCTTCCAAATAATAAACCTAAATCTA
TGTCACTATGAAGATGGTTAATGAACCTATTAACAAAATGATGGTACAT
ATAGCATTATTAAGAACTTTATTAGATCGACAAGGAAATATTGTAGCA
CAAGAGATTGTATCAGACACTTTAAACCAACAAATCAAAATCTACAAA
AATCAACCTGTAACTACAATTCAAAAAACAAATTACCAATTTACAG
CTATTAACTTATGAGAAATTTATGGCAACCATCAAACTCCACTACTGTA
AAATCAAAACA

SEQ ID NO. 7104

STRAIN H36B

CCAAGTCCGTGTCCAAGTTATAGGCGTCAATGACTTTTATGGTGCATTG
ACAATCTGGAACAGCAAATATGCTGACGGAAGTTACTAATGCTGGC
ACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAGATTTCAA
ACAAACTAACCTTAATGGTGAAGCATTAGAGTTCAAGCTGGTGAATGG
TTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTT
AAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGA
ATTTGATGAAGTTTGGCAGAATCAATCGTATCGTTACTGGAAAGGCC
CTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACAGAA
GCTGCAAAACAAGAAATTTGATGTCGCAACGTTATTGATAAAGTTAACAA
ACAAATCCCTTACAAATGGAAACCTTACACTATTAAAAATATTCTGTAA
ATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATC
CCAAACCTTGTCTTACGTAAAAATATGAACAAATGAATTTTATAGATGA
AGCTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAATGTCA
AGGCTATTGTAGTCCCTGCTCATGTACCTGCAACAAGCAAGGATGATATT
GCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCC
TGAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAA
ATGCTCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAA
GCCTATGCTGATGTACGTGGTGTCTTATAGTACTGATACACAAGATTTCAT
TGAAACCCCTTCAGCTAAAGTAAATGTCAGTTGCTCCTGGTAAAAAACAG
GTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAA
CAAGTAACAGAAAGCTAAAAATGGTACTGCCGAGGTAAGTGGCATGATTAC
CGCTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCCTCATCACAG
AGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGGC
ATGACAAATAATGGTGGCATTGCTGCTGACTTACTCATCAACAGATGG
AACAATCACTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCT
TACAAGTCTGCGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGAA
CAATACGACCAAAACAAATTTCTTCTTCAAATAGCTGGTCTGCGATA
CACTTACACAGATAATAAGAGGGCGGGGAAGAAACCACTTTAAAGTTG
TAAAGCTTTATAAATCAAATGGTGAAGAAATCAATCCTGATGCAAAATAC
AAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAG
CTTCAGAAATGCCAACTTCTAGGAGCCATTAATCCCGATACAGAGGTAT
TTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAAGCTT
CCAAATAATAAACCCTAAATCTATGTCACTATGAAGATGGTTAATGAAAC
TATTACCAAAATGATGGTACATATAGCATTTATTAAGAACTTTATTTAG
ATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTAAAC
CAACAAATCAAAATCTACAAAAATCAACCTGTAACTACAATTCACAA
AAAACAATTACACCAATTTACAGCTATTAAACCTATGAGAAATTTATGGCA
AACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7105

STRAIN 18RS21

GACCAAGTCCGTGTCCAAGTTATAGGCGTCAATGACTTTT
ATGGTGCATTGACAATACTGGAACAGCAAATATGCTGACGGAAGTT
AnTAATGCTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCA

Table 71: Comparative Sequences relating to SAG1333

AAAAGATTTCAAACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAG
 CTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGAT
 GAACCAACCGTTAAACATTTAATGCAATGAATGTTGAGTATGGCATT
 AGGTAACCATGAATTTGATGAAGTTTGGCAGAATACAACTCGTATCGTTA
 CTGGAAAGGCCCTGCTCCAGATTCTAATATAAATAATATACGAAATCA
 TACCCACACGAAGCTGCAAAACAAGAAATTTAGTAGGCAACGTTATTGA
 TAAAGTTAAACAAACAAATCCCTTACAATTTGGAACCTTACACTATTAAAA
 ATATTCTCTGTAAATAACAAAGTGTGAACGTTGGCTTTATCGGAATCGTT
 ACCAAAGACATCCCAACCTTGTCTTACGTAAAAATTTATGAACATATGA
 ATTTTTAGATGAAGCTGAACAATCGTTAAATACGCCAAAGAATTACAAG
 CTAAAAATGTCAAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGC
 AAGGATGATATGTCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAA
 TCAACTCTTCCCTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATC
 ATCAATATACAAATGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTC
 TCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGTCTTAGATACTGATAC
 ACAAGATTTCATTGAAACCCCTTCAGCTAAAGTAAITGCAAGTTGCTCCTG
 GTAAAAAACAGGTTAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAAT
 ACTATCGTTAAACAAGTAACAGAAGCTAAAAATTGGTACTGCCGAGGTAAG
 TGGCATGATTACGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCA
 GCCTCATCACAGAGGCTCACTAGCAATTTGCTCGAAAAGCTGGCCAGAT
 ATCGATTTTGCCATGACAAATAATGGTGGCATTGCTGCTGACTTACTCAT
 CAAACAGATGGAACAATCACTGGGGAGCTGCACAAGCAGTTCAACCTT
 TTGGTAATATCTTACAAGTCGTGCAAAATTAAGTAGAGATCTTTATAAA
 GCACTCAACGAACAATACGACCAAAAACAAAATTTCTTCTTCAAAATAGC
 TGGTCTGCGATACACTTACACAGATAATAAGAGGGCGGGGAAGAAACAC
 CATTTAAAGTTGTAAGCTTATAAATCAAATGGTGAGGAATCAATCCT
 GATGCAAAATACAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGA
 TGGCTTTGCAAGCTTCAGAAATGCCAAATCTTAGGAGCCATTATCCCG
 ATACAGAGGTATTTATGGCCATATATCACTGATTAGAAAAAGCTGGTAAA
 AAGGTAGCGTTCCAAATAATAAACCCTAAATCTATGCTCACTATGAAGAT
 GGTTAATGAACTATTACACAAAATGATGGTACATATAGCATTATTAAGA
 AACTTTATTTAGATCGACAAGGAATATTGTAGCACAAGAGATTGTATCA
 GACCTTTAAACCAACAAATCAAATCTACAAAAATCAACCCGTGAAC
 TACAATTCACAAAAACAATTAACCAATTTACAGCTATTAAACCTATGA
 GAAATTATGGCAAACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7106

STRAIN M732

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTT
 GACAATACCTGGAACAGCAAAATATGCTGACGGAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTC
 AACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG
 GTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGT
 TAAAAATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATG
 AATTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCC
 CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
 AGCTGCAAAACAAGAAATTTAGTGGCAACGTTATTGATAAAGTTAACA
 AACAAATCCCTTACAATTGGAACCTTACACTATTAAAAATATTCTGTGA
 AATAACAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACAT
 CCCAAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTATAGT
 AAGCTGAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
 AAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATAT
 TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCC
 CTGAAAAATAGCGTAGATATTGTCTTGTCTGGACACAATCATCAATATACA
 AATGGTCTTGTGTTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
 AGCCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTC
 TTGAAACCCCTTCAGCTAAAGTAATTGCAAGTTGCTCTCTGGTAAAAAACA
 GGTAGTGCCGATATTCAAGCAATTTGTTGACCAAGCTAATACTACTGTTAA
 ACAAGTAACAGAAGCTAAAAATGGTACTGCCGAGGTAAGTGGCATGATTA
 CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
 GAGGCTCAACTAGCAATTGCTCGAAAAGCTGGCCAGATATCGATTTTGC
 CATGACAAATAATGGTGGCATTGCTGCTGACTTACTCATCAAACAGATG
 GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
 TTACAAGTCGTGAAATTAAGTGGTAGAGATCTTTATAAGCACTCAACGA
 ACAATACGACCAAAAACAATAATTTCTTCTTCAATAGCTGGTCTGCGAT
 ACCTTACACAGATAATAAGAGGGCGGGGAAGAAACACCAATTTAAAGTT
 GTAAAGCTTATAAATCAATGGTGAGGAAATCAATCTGATGCAAAATA
 CAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTATGGCTTTGCAA
 GCTTCAGAAATGCCAACTTCTAGGAGCCATTATCCCGATACAGAGGTA
 TTTATGGCCATATCACTGATTAGAAAAAGCTGGTAAAAAAGTGAGCAT
 TCCAAATAATAAACCTAAAAATCTATGTCACTATGAAGATGGTAAATGAAA
 CTATTACACAAAATGATGGTACATATAGCATTATTAAGAAACTTTATTTA
 GATCGACAAGGAATATTGTAGCACAAGAGATTGTATCAGACACTTTAA
 CCAACAAAAATCAAATCTACAAAAATCAACCCGTGAACCTACAAATTCACA
 AAAAAAATTAACCAATTTACAGCTATTAAACCTATGAGAAATTATGGC
 AACCATCAAACTCCACTACTGTAAATCAAAACAA

SEQ ID NO. 7107

STRAIN COH1

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTT
 GACAATACCTGGAACAGCAAAATATGCTGACGGAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTC
 AACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG

Table 71: Comparative Sequences relating to SAG1333

GTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGT
 TAAAAACATTAAATGCAATGAATGTTGAGTATGGCACAATTAGGTAACCATG
 AATTGTAGTAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCC
 CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
 AGCTGCAAAACAAGAAATTTAGTGGCAAACGTTATTGATAAAGTTAACA
 AACAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCTGTGA
 AATAACAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACAT
 CCCAAACCTTGTCTTACGTAAAAATATGAACAATATGAATTTTATGATG
 AAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
 AAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATAT
 TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCC
 CTGAAAAATAGCGTAGATATTGTCTTGTCTGGACACAATCATCAATATACA
 AATGGTCTTGTGGTAAACTCGTATTGTACAAAGCGCTCTCTCAAGGAAA
 AGCCTATGCTGATGTACGTGGTGTCTAGATACTGATACACAAGATTCA
 TTGAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACA
 GGTAGTGCCGATATTCAAGCCATTGTGACCAAGCTAATACTATCGTTAA
 ACAAGTAACAGAAGCTAAAAATGGTACTGCCAGGTAAGTGGCATGATTA
 CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
 GAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGC
 CATGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAAACAGATG
 GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
 TTACAAGTCGTGCAAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGA
 ACAATACGACCAAAAAACAATAATTTCTTCTTCAATAGCTGGTCTGCGAT
 ACACCTTACACAGATAATAAGAGGGCGGGGAAGAAACACCATTAAAGTT
 GTAAAGCTTATAAATCAAAATGGTGAAGAAATCAATCTGATGCAAAATA
 CAAATTAGTTATCAATGACTTTTATTCTGGTGGTGGTGGTGGCTTTGCAA
 GCTTCAGAAATGCCAACTTCTAGGAGCCATTATCCGATACAGAGGTA
 TTTATGGCCTATATCACTGATTAGAAAAAGCTGGTAAAAAGTGGAGCAT
 TCCAAATAATAAACCCTAAAAATCTATGTCACTATGAAGATGGTTAATGAAA
 CTATTACACAAAATGATGGTACATATAGCATTATTAAGAACTTTATTTA
 GATCCGACAAGGAAATATGTAGCACAAAGAGATTGTATCAGACACTTTAA
 CCAACCAAAATCAAAATCTACAAAATCAACCTGTAACTACAATTCA
 AAAAAAATTACCAAAATTTACAGCTATTAAACCTATGAGAAATTATGGC
 AAACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7108

STRAIN M781

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACCTTGA
 CAATACTGGAACAGCAAAATATGCCTGACGGAAGTTACTAATGCTGGCA
 CTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAA
 CAACTAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGGATATGGT
 TGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTA
 AAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAA
 TTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCCCC
 TGCTCCAGATTCTAATAATAAATAATATTACGAAATCATACCCACACGAAG
 CTGCAAAAACAAGAAATGTAGTGGCAAACGTTATTGATAAAGTTAACAAA
 CAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCTGTAAA
 TAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATCC
 CAAACCTTGTCTTACGTAAAAATTAAGAACATATGAATTTTATGATGAA
 GCTGAAACAATCGTTAATAACGCCAAAGAAATTAAGCTAAAAATGTCAA
 GGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATATTG
 CTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCT
 GAAAAATAGCGTAGATATTGTCTTGTCTGGACACAATCATCAATATACAAA
 TGGTCTTGTGGTAAACTCGTATTGTACAAAGCGCTCTCTCAAGGAAAAG
 CCTATGCTGATGTACGTGGTGTCTTAGATACGATACACAAGATTTCATT
 GAAACCCCTTCAGCTAAAGTAATTCAGTTGCTCCTGGTAAAAAACAAGG
 TAGTGCCGATATTCAAGCCATTGTGACCAAGCTAATACTATCGTTAAAC
 AAGTAACAGAAGCTAAATTTGGTACTGCCAGGTAAGTGGCATGATTACG
 CGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
 GGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
 TGACAAATAATGGTGGCATTCTGTGCTGACTTACTCATCAACCCAGATGGA
 ACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
 ACAAGTCGTGCAAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGAAC
 AATACGACCAAAAAACAATAATTTCTTCTTCAATAGCTGGTCTGCGATAC
 ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTAAAGTTGT
 AAAAGCTTATAAATCAATGGTGAAGAAATCAATCCTGATGCAAAATACA
 AATTAGTTATCAATGACTTTTATTCTGGTGGTGGTGGTGGCTTTGCAAGC
 TTCAGAAATGCCAACTTCTAGGAGCCATTATCCCGATACAGAGTATT
 TATGGCTTATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGGCATTC
 CAAATAATAAACCTAAAAATCTATGTCACTATGAAGATGGTTAATGAACT
 ATTACAAAAATGATGGTACATATAGCATTATTAAAGAACTTTATTAGAA
 TCGACAAGGAAATATGTAGCACAAAGAGATTGTATCAGACACTTTAAACC
 AAACAAAATCAAAATCTACAAAATCAACCTGTAACTACAATTCAAAA
 AAACAATTACACCAATTTACAGCTATTAAACCTATGAGAAATTATGGCAA
 ACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7109

STRAIN CJB110

GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGC
 ACTTGACAATACTGGAACAGCAAAATATGCCTGACGGAAGTTACTAATG
 CTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGAT
 TTCAAAACAACTAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGA
 TATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAA

Table 71: Comparative Sequences relating to SAG1333

CCGTTAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAAC
 CATGAATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAG
 GGCCCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCAC
 ACGAAGCTGCAAAACAGAAATTTAGTGGCAACCGTTATGTATAAAGTT
 AACAAACAAATCCCTTACAATTGGAACCTTACGCTATTAAAAATATTCC
 TGTAAATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAG
 ACATCCCAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTAA
 GATGAAGCTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAA
 TGTCAAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATG
 ATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTC
 TTCCTTGAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATA
 TACAAATGGTCTTGTGGTAAAACTCGCATTGTACAAGCGCTCTCTCAAG
 GAAAAGCCTATGCTGACGTACGTGGTGTCTAGATACTGATACACAAGAT
 TTCATTGAAACCCCTTACGCTAAAGTAGTTGCGATTGCTCTCTGGTAAAA
 AACAGGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATATCTATCG
 TTAACAAGCTGAAACAAGCTAAAAATGGTACTGCCGAGGTAAAGTGGCATG
 ATTACGCGTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCAGCGCTCAT
 CACAGAGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATT
 TTGCCATGACAAATAATGGTGGCATTCTGTGCTGACTTACTCATCAAAACCA
 GATGGAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAA
 TATCTTACAAGTCTGTCGAAATTAAGTGGTAGAGATCTTTATAAGCACTCA
 ACGAACATACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTG
 CGATACACTTACACAGATAATAAAGAGGGCGGAGAGAAACACCATTTAA
 AGTTGTAAAAGCTTATAAATCAAAATGGTGAAGAAATCAATCTGTATGCAA
 AATACAAATAGTTATCAATGACTTTTATTCTGGTGGTGGTATGGCTTT
 GCAAGCTTCAGAAATGCAAACTTCTAGGAGCCATTAAATCCGATACAGA
 GGTATTTATGGCTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGA
 GCGTTCCAAATAATAAACCTAAAAATCTATGTCACTATGAAGATGGTTAAT
 GAACTATTACACAAATGATGGTACACATAGCATTATTAAGAACTTTA
 TTTAGATCGACAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTT
 TAAACCAAAACAAATCAAAATCTACAAATCAACCTGTAACTACAAAT
 CACAAAAACAATTACACCAATTTACAGCTATTAACCTATGAGAAATTA
 TGGCAACCATCAAACTCCACTACTGTAAATCA

SEQ ID NO. 7110

STRAIN 1169NT

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGA
 CAATACTGGAACAGCAAAATATGCCCTGATGGAAGAGTTGCTAATGCTGGTA
 CTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAA
 CAAACTAACCCCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGT
 TGGAGCAAGTCCAGCCAACTCTGGCTTCTTCAAGATGAACCAACTGTGCA
 AAAATTTTAAATGCAATGAATGTTGAGTATGGCACATTGGGTAAACATGAA
 TTTGATGAAGGGTTGGCAGAAATATAATCGTATCGTTACTGGTAAAGCCCC
 TGCTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACATGAAG
 CTGCAAAACAAGAAATTTAGTGGCAAAATGTTATGATAAGTTTAAACAA
 CAAATTCCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCCTGTAA
 TAACAAAGTGTGAACGTTGGCTTTATCGGGATTGTCACCAAGACATCC
 CAAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTATGATGAA
 GCTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAATGTCAA
 AGCTATTGTAGTCTCGCACATGTACCTGCAACAAGTAAAAATGATATTG
 CTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCT
 GAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
 TGGTCTTGTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAAG
 CCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTCATT
 GAGACCCCTTCACTAAAGTAATTGCAGTTGCTCTCTGGTAAAAAACAGG
 TAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAAC
 AAGTAACAGAAGCTAAATTTGGTACTGCCGAGGTAAGTGTATGATTACG
 CGTTCTGTTGATCAAGATAATGTTAGTCCGCTAGGCAGCCTCATCACAGA
 GGTCAACTAGCAATTTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
 TGACAAATAATGGTGGCATTCTGTCTGACTTACTCATCAAACAGATGGA
 ACAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
 ACAAGTCGTCGAAATTAAGTGGTAGAGATCTTTATAAGCACTCAACGAAC
 AATACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTGCGATAC
 ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGT
 AAAAGCTTATAAATCAAAATGGTGAAGGAAATCAATCCTGATGCAAAATACA
 AATTAGTTATCAATGACTTTTATTCTGGTGGTGGTATGGCTTTGCAAGC
 TTCAGAAATGCCAACTTCTAGGAGCCATTAAACCCGATACAGAGGTATT
 TATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGAAGCGTTT
 CAAATAATAAACCTAAATCTATGTCACTATGAAGATGGTTAATGAACT
 ATTTACAAAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGA
 TCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACC
 AAACAAATCAAAATCTACAAAAATCAACCTGTAACTACAAATCACAAA
 AAACAATTACACCAATTTACAGCTATTAACCCCTATGAGAAATTTGGCAA
 ACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7111

STRAIN JM9130013

CGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGACAATA
 CTGGAACAGCAAAATATGCCCTGACGGAAGGTTACTAATGCTGGCACTGCT
 GCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAACAAAC
 TAACCCCTAATGGTGAAGCAATTAGAGTTCAAGCTGGTATGATGGTTGGAG
 CAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTAAACCA
 TTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAAACCATGAATTTGA

Table 71: Comparative Sequences relating to SAG1333

TGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCTGCTC
 CAGATTcTAATATAAATAATATTACGAAATCATACCCACACGAAGCTGCA
 AAACAAGAAATTTAGTGGCAACGTTATTTGATAAAGTTAAACAAACAAAT
 CCCTTACAATTTGGAACCTTACACTATTAATAATATTCTGTAAATAACA
 AAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCCCAAAC
 CTGTCTTACGTAAAAATTATGAACAATATGAATTTTGTAGATGAAGCTGA
 AACAAATCGTTAAATACGCCAAAGAATTACAGCTAAAAATGTCAAGGCTA
 TTGTAGTCTTGTCTCATGTACCTGCAACAGCAAGGATGATATTGCTGAA
 GGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTGAAAA
 TAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAATGGTC
 TTGTTGGTAAAACTCGTATTGTACAGCGCTCTCTCAAGGAAAAGCCTAT
 GCTGATGTACGTGGTGTCTAGATACCTGATACACAAGATTTTATTGAAAC
 CCCTTCAGCTAAAGTAATTGCAAGTTGCTCCTGGTAAAAAACAGGTAGTG
 CCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACAAGTA
 ACAGAAGCTAAAAATTTGGTACTGCCGAGGTAAAGTGGCATGATTACGCGTTC
 TGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTC
 AACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGAATTTGCCATGACA
 AATAATGGTGGCATTCTGTCTGACTTACTCATCAAACAGATGGAACAAT
 CACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTACAAG
 TCGTGCAGAAATTAATGGTAGATCTTTATAAAGCACTCAACGAACAATAC
 GACCAAAAAACAAATTTCTTCTTCAAAATAGCTGGTCTGCGATACACTTA
 CACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAG
 CTTATAAATCAAAATGGTGAAGAAATCAATCCTGATGCAAAATACAAATTA
 GTTATCAATGACTTTTATTCTGGTGGTGGTGGTGGCTTTGCAAGCTTCAG
 AAATGCCAACTCTTAGGAGCCATTAATCCCGATACAGAGGTATTATGG
 CCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCCAAT
 AATAAACCTAAAACTATGTCACTATGAAGATGGTTAATGAACTATTAC
 ACAAAATGATGGTACATATAGCATTATTGAGAACTTTATTTAGATCGAC
 AAGGAAATATTGTAGCACAAAGAGATTGTATCAGACACTTTAAACCAAACA
 AAATCAAAATCTACAAAATCAACCTGTAACCTACAATTACAAAAAACA
 ATTACCAATTTACAGCTATTAAACCTATGAGAAATTTATGGCAACCAT
 CAACTCCACTACTGTAAATCAAAA

PRETTY of: /biotmp/msa237456.2{*} May 14, 2003 03:20 ..

	1				50
msa237456.2{328_1169NT}	-----	-----	-----	-----	-----
msa237456.2{328_2603}	atgaaaaaga	aaattattht	gaaaagtagt	gttcttggtt	tagtcgctgg
msa237456.2{328_18RS21}	-----	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa237456.2{328_1169NT}	-----	-----	-----	-----	-----
msa237456.2{328_2603}	gacttctatt	atgttctcaa	gcgtgttcgc	gGACcaagtc	ggtgtccaag
msa237456.2{328_18RS21}	-----	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa237456.2{328_1169NT}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_2603}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_18RS21}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_H36B}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_COH1}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_M732}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_M781}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_JM9130013}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_A909}	-----GCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_090}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_CJB110}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
Consensus	-----****	*****	*****	*****	*****
	151				200
msa237456.2{328_1169NT}	AATATGCCTG	AtGGAAAAAGT	TgcTAATGCT	GGtACTGCTG	CTCAATTAGA
msa237456.2{328_2603}	AATATGCCTG	AtGGAAAAAGT	TgcTAATGCT	GGtACTGCTG	CTCAATTAGA
msa237456.2{328_18RS21}	AATATGCCTG	AcGGAAAAAGT	TanTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_H36B}	AATATGCCTG	AcGGAAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_COH1}	AATATGCCTG	AcGGAAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_M732}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_M781}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_JM9130013}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_A909}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_CJB110}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
Consensus	*****	*-*****	*-*****	*-*****	*****
msa237456.2{328_1169NT}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_2603}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_18RS21}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_H36B}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_COH1}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_M732}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_M781}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_JM9130013}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_A909}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_090}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_CJB110}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_2603}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_18RS21}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_H36B}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_COH1}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_M732}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_M781}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_JM9130013}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_A909}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_090}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_CJB110}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_2603}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_18RS21}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_H36B}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_COH1}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_M732}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_M781}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_JM9130013}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_A909}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_090}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_CJB110}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_2603}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_18RS21}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_H36B}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_COH1}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_M732}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_M781}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_JM9130013}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_A909}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_090}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_CJB110}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CAGAATAcAA	TCGTATCGTT	ACTGGtAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_2603}	CAGAATAcAA	TCGTATCGTT	ACTGGtAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_18RS21}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_H36B}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_COH1}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_M732}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_M781}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_JM9130013}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_A909}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_090}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_CJB110}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	ATtAATAATA	TTACGAAATC	ATACCCACat	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_2603}	ATtAATAATA	TTACGAAATC	ATACCCACat	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_18RS21}	ATaAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_H36B}	ATaAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_COH1}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_M732}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_M781}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_JM9130013}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_A909}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_090}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_CJB110}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	501	TGTAAGTTAA	ATAAAGTTAA	CAAACAAATc	550
msa237456.2{328_2603}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_18RS21}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_H36B}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_COH1}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_M732}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_M781}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_JM9130013}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_A909}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_090}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_CJB110}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	551	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	600
msa237456.2{328_2603}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_18RS21}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_H36B}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_COH1}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_M732}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_M781}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_JM9130013}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_A909}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_090}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_CJB110}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	601	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	650
msa237456.2{328_2603}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_18RS21}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_H36B}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_COH1}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_M732}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_M781}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_JM9130013}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_A909}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_090}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_CJB110}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	651	TAAAAATTAT	GAACAATATG	AATTTTTAGA	700
msa237456.2{328_2603}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_18RS21}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_H36B}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_COH1}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_M732}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_M781}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_JM9130013}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_A909}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_090}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_CJB110}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	701	AATACGCCAA	AGAATTACAA	GCTAAAAATG	750
msa237456.2{328_2603}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
msa237456.2{328_18RS21}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
msa237456.2{328_H36B}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
msa237456.2{328_COH1}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
msa237456.2{328_M732}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
msa237456.2{328_M781}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
msa237456.2{328_JM9130013}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
msa237456.2{328_A909}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
msa237456.2{328_090}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
msa237456.2{328_CJB110}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	751	GCaCATGTAC	CTGCAACAAG	tAAaaATGAT	800
msa237456.2{328_2603}	GCaCATGTAC	CTGCAACAAG	tAAaaATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_18RS21}	GCtCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_H36B}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_COH1}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_M732}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_M781}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_JM9130013}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_A909}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_O90}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_CJB110}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
Consensus	***-*****	*****	-*-**	*****	*****
msa237456.2{328_1169NT}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_2603}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_18RS21}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_H36B}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_COH1}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_M732}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_M781}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_JM9130013}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_A909}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_O90}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_CJB110}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_2603}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_18RS21}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_H36B}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_COH1}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_M732}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_M781}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_JM9130013}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_A909}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_O90}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_CJB110}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_2603}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_18RS21}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_H36B}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_COH1}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_M732}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_M781}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_JM9130013}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_A909}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_O90}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_CJB110}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_2603}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_18RS21}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_H36B}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_COH1}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_M732}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_M781}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_JM9130013}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_A909}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_O90}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_CJB110}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_2603}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_18RS21}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_H36B}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_COH1}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_M732}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_M781}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_JM9130013}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_A909}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_O90}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_CJB110}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_2603}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_18RS21}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_H36B}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_COH1}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_M732}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_M781}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_JM9130013}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_A909}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_090}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_CJB110}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AATTGGTACT	GCCGAGGTAA	GTGtCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_2603}	AATTGGTACT	GCCGAGGTAA	GTGtCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_18RS21}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_H36B}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_COH1}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_M732}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_M781}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_JM9130013}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_A909}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_090}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_CJB110}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
Consensus	*****	*****	***_*****	*****	*****
msa237456.2{328_1169NT}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_2603}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_18RS21}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_H36B}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_COH1}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_M732}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_M781}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_JM9130013}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_A909}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_090}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_CJB110}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
Consensus	*****	***_*****	*****	*****	*****
msa237456.2{328_1169NT}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_2603}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_18RS21}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_H36B}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_COH1}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_M732}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_M781}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_JM9130013}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_A909}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_090}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_CJB110}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_2603}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_18RS21}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_H36B}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_COH1}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_M732}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_M781}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_JM9130013}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_A909}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_090}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_CJB110}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_2603}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_18RS21}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_H36B}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_COH1}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_M732}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_M781}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_JM9130013}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_A909}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_090}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_CJB110}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	ACTGGTAGAG	ATCTTTTATA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
Consensus	*****	*****	*****	*****	*****

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_2603}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_18RS21}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_H36B}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_COH1}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_M732}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_M781}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_JM9130013}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_A909}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_090}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_CJB110}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_2603}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_18RS21}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_H36B}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_COH1}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_M732}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_M781}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_JM9130013}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_A909}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_090}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_CJB110}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAGAGC	TTATAAATCA
msa237456.2{328_2603}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAGAGC	TTATAAATCA
msa237456.2{328_18RS21}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAGAGC	TTATAAATCA
msa237456.2{328_H36B}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAGAGC	TTATAAATCA
msa237456.2{328_COH1}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAGAGC	TTATAAATCA
msa237456.2{328_M732}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAGAGC	TTATAAATCA
msa237456.2{328_M781}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAGAGC	TTATAAATCA
msa237456.2{328_JM9130013}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAGAGC	TTATAAATCA
msa237456.2{328_A909}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAGAGC	TTATAAATCA
msa237456.2{328_090}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAGAGC	TTATAAATCA
msa237456.2{328_CJB110}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAGAGC	TTATAAATCA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_2603}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_18RS21}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_H36B}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_COH1}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_M732}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_M781}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_JM9130013}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_A909}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_090}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_CJB110}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_2603}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_18RS21}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_H36B}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_COH1}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_M732}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_M781}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_JM9130013}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_A909}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_090}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_CJB110}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_2603}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_18RS21}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_H36B}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_COH1}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M732}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M781}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_JM9130013}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_A909}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_090}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_CJB110}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_2603}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_18RS21}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_H36B}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_COH1}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M732}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M781}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_JM9130013}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_A909}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_090}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_CJB110}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
Consensus	*****	*****	*****	*****	*****

1651

1700

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_1169NT}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_2603}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_18RS21}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_H36B}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_COH1}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_M732}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_M781}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_JM9130013}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_A909}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_090}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_CJB110}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
Consensus	*****	*****	*****	-*****	*****
msa237456.2{328_1169NT}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_2603}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_18RS21}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_H36B}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_COH1}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_M732}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_M781}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_JM9130013}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_A909}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_090}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_CJB110}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_2603}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_18RS21}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_H36B}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_COH1}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_M732}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_M781}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_JM9130013}	GTACACATAG	CATTATTgAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_A909}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_090}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_CJB110}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_2603}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_18RS21}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_H36B}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_COH1}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_M732}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_M781}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_JM9130013}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_A909}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_090}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_CJB110}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_2603}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_18RS21}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_H36B}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_COH1}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_M732}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_M781}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_JM9130013}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_A909}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_090}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_CJB110}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_2603}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_18RS21}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_H36B}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_COH1}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_M732}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_M781}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_JM9130013}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_A909}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_090}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_CJB110}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
Consensus	*****	*****	*****	*****	*****

Table 71: Comparative Sequences relating to SAG1333

	1951			2000
msa237456.2{328_1169NT}	ACTGTAAAT CAAA-----	-----	-----	-----
msa237456.2{328_2603}	ACTGTAAAT CAAAACAAtt	acccaaaaaca	aactctgaat	atggacaatc
msa237456.2{328_18RS21}	ACTGTAAAT CAAA-----	-----	-----	-----
msa237456.2{328_H36B}	ACTGTAAAT CAAA-----	-----	-----	-----
msa237456.2{328_COH1}	ACTGTAAAT CAAA-----	-----	-----	-----
msa237456.2{328_M732}	ACTGTAAAT CAAAACAA--	-----	-----	-----
msa237456.2{328_M781}	ACTGTAAAT CAAA-----	-----	-----	-----
msa237456.2{328_JM9130013}	ACTGTAAAT CAAA-----	-----	-----	-----
msa237456.2{328_A909}	ACTGTAAAT CAAAACAA--	-----	-----	-----
msa237456.2{328_090}	ACTGTAAAT CAAAACAA--	-----	-----	-----
msa237456.2{328_CJB110}	ACTGTAAAT CA-----	-----	-----	-----
Consensus	***** **_*****	*****	*****	*****
	2001			2050
msa237456.2{328_1169NT}	-----	-----	-----	-----
msa237456.2{328_2603}	attccttatg	tctgtctttg	gtgttggaact	tataggaatt
msa237456.2{328_18RS21}	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----
Consensus	*****	*****	*****	*****
	2051			2070
msa237456.2{328_1169NT}	-----	-----	-----	-----
msa237456.2{328_2603}	caaagaaaaa	acatatgaaa	-----	-----
msa237456.2{328_18RS21}	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----
Consensus	*****	*****	-----	-----

SEQ ID NO. 7112

STRAIN 2603 frame: 1

MKKKIILKSSVLGLVAGTSIMFSSVFADQVGQVIGVNDPHGALDNTGTANMPDGKVVANA
 GTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVGASPANSGLLQDEPTVKNFNAMNVE
 YGTLGNHEFDEGLAEYNRIVTGKAPAPDSNINNITKSPHEAAKQEIIVVANVIDKVNKQI
 PYNWKPYAIKNI PVNNKSVNVGFIGIVTKDIPNLVLRKNYEQYEFLEDEAETIVKYAKELQ
 AKNVKAIIVLAHVAPATSKDDIAEGEAAEMMKVNLFPENSVDIVFAGHNHQYTNGLVGK
 TRIVQALSQKQAYADVRGVLDTDTQDFIETPSAKVIAVAPGKKTGSADIQAIVDQANTIV
 KQVTEAKIGTAEVSGMITRSVDQDNVSPVGSGLITEAQLAIARKSWPIDFAMTNNGGIRAD
 LLIKPDGTITWGAAQAVQPFNGILQVVEITGRDLYKALNEQYDQKQNFLLQIAGLRYTY
 TDNKEGGEETPFKVVKAYKSNGBEINPDACYKLVINDFLFGGDDGFASFRNAKLLGAINP
 DTEVFMAIYITDLEKAGKKVSVPNKPKIYVTMKNVNETITQNDGTHSIIKKLYLDRQGN
 VAQEI VSDTLNQT KSKSTKINPVTTIHKQLHQFTA INPMRNYGKPSNSTTVKSKQLPKT
 NSEYQSFLMSVFGVGLIGIALNTKKHKM

SEQ ID NO. 7113

STRAIN 090 frame: 3

VGVQVIGVNDPHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRV
 QAGDMVGASPANSGLLQDEPTVKTNFAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPDS
 NINNITKSPHEAAKQEIIVVANVIDKVNKQIPYNWKPYAIKNI PVNNKSVNVGFIGIVTK
 DIPNLVLRKNYEQYEFLEDEAETIVKYAKELQAKNVKAIIVLAHVAPATSKDDIAEGEAAEM
 MKVNLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQKQAYADVRGVLDTDTQDFIET
 PSKVVAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPV
 GGLITEAQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFNGILQVVE
 ITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGBEINPD
 KYKLVINDFLFGGDDGFASFRNAKLLGAINPDTEVFMAIYITDLEKAGKKVSVPNKPKIY
 VTMKNVNETITQNDGTHSIIKKLYLDRQGNIVAQEI VSDTLNQT KSKSTKINPVTTIHK
 QLHQFTA INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7114

STRAIN A909 frame: 3

VNDPHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVG
 ASPANSGLLQDEPTVKTNFAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPDSNINNITK
 SYPHEAAKQEIIVVANVIDKVNKQIPYNWKPYAIKNI PVNNKSVNVGFIGIVTKDIPNLV
 RKNYEQYEFLEDEAETIVKYAKELQAKNVKAIIVLAHVAPATSKDDIAEGEAAEMMKVNL
 FPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQKQAYADVRGVLDTDTQDFIETPSAKVI
 AVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVGSGLITEA
 QLAIAARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFNGILQVVEITGRDLY
 KALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGBEINPDACYKLVIN
 DFLFGGDDGFASFRNAKLLGAINPDTEVFMAIYITDLEKAGKKVSVPNKPKIYVTMKNV
 NETITQNDGTHSIIKKLYLDRQGNIVAQEI VSDTLNQT KSKSTKINPVTTIHKQLHQFTA

Table 71: Comparative Sequences relating to SAG1333

INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7115

STRAIN H36B frame: 2

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQVV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTDNKEGGEETPFKVVKAYKSNNGEINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVNNKPKI
 YVTMKNVNETITQNDGTYSI I KKL YLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7116

STRAIN 18RS21 frame: 1

DQVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
 RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIV
 TKDI PNLVLRKNYEQYEFLEDAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAA
 EMMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQKAYADVRGVLDTDQDFI
 IETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVS
 PVGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQVV
 VEITGRDLYKALNEQYDQKQNFLLQIAGLRITYTDNKEGGEETPFKVVKAYKSNNGEINPD
 DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVNNKPKI
 IYVTMKNVNETITQNDGTYSI I KKL YLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKSK

SEQ ID NO. 7117

STRAIN M732 frame: 3

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQVV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTDNKEGGEETPFKVVKAYKSNNGEINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVNNKPKI
 YVTMKNVNETITQNDGTYSI I KKL YLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7118

STRAIN COH1 frame: 3

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQVV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTDNKEGGEETPFKVVKAYKSNNGEINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVNNKPKI
 YVTMKNVNETITQNDGTYSI I KKL YLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7119

STRAIN M781 frame: 1

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQVV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTDNKEGGEETPFKVVKAYKSNNGEINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVNNKPKI
 YVTMKNVNETITQNDGTYSI I KKL YLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7120

STRAIN CJB110 frame: 1

DQVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
 RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIV
 TKDI PNLVLRKNYEQYEFLEDAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAA
 EMMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQKAYADVRGVLDTDQDFI
 IETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVS
 PVGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQVV
 VEITGRDLYKALNEQYDQKQNFLLQIAGLRITYTDNKEGGEETPFKVVKAYKSNNGEINPD

Table 71: Comparative Sequences relating to SAG1333

DAKYKLIVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPK
IYVTMKNVNETITQNDGTHSIKKLYLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7121

STRAIN 1169NT frame: 1

QVGQVIGVNDVDFHGLDNTGTANMPDGKVNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKFNAMNVEYGTIGNHEFDEGLAEYNRI VTGKAPAPD
SNINNITKSYPHAEAKQEI VVANVIDKVNKQI PYNWKPYAIKNI PVNNKSVNVGFIGIVT
KDI PNVLVRKNYEQYEFLEDEARTI VKYAKELQAKNVKAI VVLAHV PATSKNDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRI VQALSQGKAYADVRGVLDTDQDFI
ETPSAKVIAVAPGKKTGSADIQAI VQDQANTIVKQVTEAKIGTAEVSMITRSVDQDNVSP
VGSILTEAQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAQAQVQPFNGILQVV
EITGRDLKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKA YKSNGEIINPD
AKYKLIVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKI
YVTMKNVNETITQNDGTHSIKKLYLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7122

STRAIN JM9130013 frame: 2

GVQVIGVNDVDFHGLDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQ
AGDMVGASPANSGLLQDEPTVKFNAMNVEYGTIGNHEFDEGLAEYNRI VTGKAPAPDSN
INNITKSYPHAEAKQEI VVANVIDKVNKQI PYNWKPYTIKNI PVNNKSVNVGFIGIVTKD
IPNLVLRKNYEQYEFLEDEARTI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAEM
KKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRI VQALSQGKAYADVRGVLDTDQDFIET
PSAKVIAVAPGKKTGSADIQAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVG
SLITEAQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAQAQVQPFNGILQVVEI
TGRDLKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKA YKSNGEIINPD
YKLIVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKIYV
TMKNVNETITQNDGTHSIKKLYLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHKQ
LHQFTAINPMRNYGKPSNSTTVKS

PRETTY of: /biotmp/msa237615.2{*} May 14, 2003 03:22 ..

	i		50
msa237615.2{328_1169NT}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_2603}	mkkkilkss vlglvagtsi mfsavfaDqv	gvqvigVNDF	HGALDNTGTA
msa237615.2{328_A909}	-----	-----VNDF	HGALDNTGTA
msa237615.2{328_M732}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_COH1}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_M781}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_H36B}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_JM9130013}	-----	-----	gvqvigVNDF HGALDNTGTA
msa237615.2{328_18RS21}	-----	-----Dqv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_090}	-----	-----v	gvqvigVNDF HGALDNTGTA
msa237615.2{328_CJB110}	-----	-----Dqv	gvqvigVNDF HGALDNTGTA
Consensus	*****	*****	*****
	51		100
msa237615.2{328_1169NT}	NMPDGKvNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_2603}	NMPDGKvNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_A909}	NMPDGKvNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_M732}	NMPDGKvNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_COH1}	NMPDGKvNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_M781}	NMPDGKvNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_H36B}	NMPDGKvNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_JM9130013}	NMPDGKvNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_18RS21}	NMPDGKvNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_090}	NMPDGKvNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_CJB110}	NMPDGKvNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
Consensus	*****	*****	*****
	101		150
msa237615.2{328_1169NT}	NSGLLQDEPT VknFNAMNVE YGTIGNHEFD	EGLAEYNRI	TGKAPAPDSN
msa237615.2{328_2603}	NSGLLQDEPT VknFNAMNVE YGTIGNHEFD	EGLAEYNRI	TGKAPAPDSN
msa237615.2{328_A909}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRI	TGKAPAPDSN
msa237615.2{328_M732}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRI	TGKAPAPDSN
msa237615.2{328_COH1}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRI	TGKAPAPDSN
msa237615.2{328_M781}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRI	TGKAPAPDSN
msa237615.2{328_H36B}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRI	TGKAPAPDSN
msa237615.2{328_JM9130013}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRI	TGKAPAPDSN
msa237615.2{328_18RS21}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRI	TGKAPAPDSN
msa237615.2{328_090}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRI	TGKAPAPDSN
msa237615.2{328_CJB110}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRI	TGKAPAPDSN
Consensus	*****	*****	*****
	151		200
msa237615.2{328_1169NT}	INNITKSYPH EAAKQEI VVA NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
msa237615.2{328_2603}	INNITKSYPH EAAKQEI VVA NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
msa237615.2{328_A909}	INNITKSYPH EAAKQEI VVA NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_M732}	INNITKSYPH EAAKQEI VVA NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_COH1}	INNITKSYPH EAAKQEI VVA NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_M781}	INNITKSYPH EAAKQEI VVA NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN

Table 71: Comparative Sequences relating to SAG1333

msa237615.2{328_H36B}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_JM9130013}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_18RS21}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_090}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
msa237615.2{328_CJB110}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
Consensus	*****	*****	*****	*****-*	*****
msa237615.2{328_1169NT}	201				250
msa237615.2{328_2603}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_A909}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_M732}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_COH1}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_M781}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_H36B}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_JM9130013}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_18RS21}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_090}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_CJB110}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	251				300
msa237615.2{328_2603}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_A909}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_M732}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_COH1}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_M781}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_H36B}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_JM9130013}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_18RS21}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_090}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_CJB110}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	301				350
msa237615.2{328_2603}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_A909}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_M732}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_COH1}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_M781}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_H36B}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_JM9130013}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_18RS21}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_090}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_CJB110}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	351				400
msa237615.2{328_2603}	AIVDQANTIV	KQVTEAKIGT	AEVSvMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_A909}	AIVDQANTIV	KQVTEAKIGT	AEVSvMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_M732}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_COH1}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_M781}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_H36B}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_JM9130013}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_18RS21}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_090}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_CJB110}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	401				450
msa237615.2{328_2603}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_A909}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_M732}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_COH1}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_M781}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_H36B}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_JM9130013}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_18RS21}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_090}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_CJB110}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	451				500
msa237615.2{328_2603}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVVKAYKS
msa237615.2{328_A909}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVVKAYKS
msa237615.2{328_M732}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVVKAYKS
msa237615.2{328_COH1}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVVKAYKS

Table 71: Comparative Sequences relating to SAG1333

msa237615.2{328_M781}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS	
msa237615.2{328_H36B}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS	
msa237615.2{328_JM9130013}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS	
msa237615.2{328_18RS21}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS	
msa237615.2{328_090}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS	
msa237615.2{328_CJB110}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS	
Consensus	*****	*****	*****	*****	*****	
501						550
msa237615.2{328_1169NT}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT	
msa237615.2{328_2603}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT	
msa237615.2{328_A909}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT	
msa237615.2{328_M732}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT	
msa237615.2{328_COH1}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT	
msa237615.2{328_M781}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT	
msa237615.2{328_H36B}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT	
msa237615.2{328_JM9130013}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT	
msa237615.2{328_18RS21}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT	
msa237615.2{328_090}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT	
msa237615.2{328_CJB110}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT	
Consensus	*****	*****	*****	*****	*****	
551						600
msa237615.2{328_1169NT}	DLEKAGKKVS	vPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi	
msa237615.2{328_2603}	DLEKAGKKVS	vPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi	
msa237615.2{328_A909}	DLEKAGKKVS	vPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi	
msa237615.2{328_M732}	DLEKAGKKVS	iPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi	
msa237615.2{328_COH1}	DLEKAGKKVS	iPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi	
msa237615.2{328_M781}	DLEKAGKKVS	iPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi	
msa237615.2{328_H36B}	DLEKAGKKVS	vPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi	
msa237615.2{328_JM9130013}	DLEKAGKKVS	vPNNKPKIYV	TMKMVNETIT	QNDGThSIie	KLYLDRQGNi	
msa237615.2{328_18RS21}	DLEKAGKKVS	vPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi	
msa237615.2{328_090}	DLEKAGKKVS	vPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi	
msa237615.2{328_CJB110}	DLEKAGKKVS	vPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi	
Consensus	*****	*****	*****	*****	*****	
601						650
msa237615.2{328_1169NT}	VAQEIVSDTL	NQTKSKSTKI	NPVTTHKKQ	LHQFTAINPM	RNYGKPSNST	
msa237615.2{328_2603}	VAQEIVSDTL	NQTKSKSTKI	NPVTTHKKQ	LHQFTAINPM	RNYGKPSNST	
msa237615.2{328_A909}	VAQEIVSDTL	NQTKSKSTKI	NPVTTHKKQ	LHQFTAINPM	RNYGKPSNST	
msa237615.2{328_M732}	VAQEIVSDTL	NQTKSKSTKI	NPVTTHKKQ	LHQFTAINPM	RNYGKPSNST	
msa237615.2{328_COH1}	VAQEIVSDTL	NQTKSKSTKI	NPVTTHKKQ	LHQFTAINPM	RNYGKPSNST	
msa237615.2{328_M781}	VAQEIVSDTL	NQTKSKSTKI	NPVTTHKKQ	LHQFTAINPM	RNYGKPSNST	
msa237615.2{328_H36B}	VAQEIVSDTL	NQTKSKSTKI	NPVTTHKKQ	LHQFTAINPM	RNYGKPSNST	
msa237615.2{328_JM9130013}	VAQEIVSDTL	NQTKSKSTKI	NPVTTHKKQ	LHQFTAINPM	RNYGKPSNST	
msa237615.2{328_18RS21}	VAQEIVSDTL	NQTKSKSTKI	NPVTTHKKQ	LHQFTAINPM	RNYGKPSNST	
msa237615.2{328_090}	VAQEIVSDTL	NQTKSKSTKI	NPVTTHKKQ	LHQFTAINPM	RNYGKPSNST	
msa237615.2{328_CJB110}	VAQEIVSDTL	NQTKSKSTKI	NPVTTHKKQ	LHQFTAINPM	RNYGKPSNST	
Consensus	*****	*****	*****	*****	*****	
651						690
msa237615.2{328_1169NT}	TVKSKQ	-----	-----	-----	-----	
msa237615.2{328_2603}	TVKSKQ	-----	-----	-----	-----	
msa237615.2{328_A909}	TVKSKQ	-----	-----	-----	-----	
msa237615.2{328_M732}	TVKSKQ	-----	-----	-----	-----	
msa237615.2{328_COH1}	TVKSKQ	-----	-----	-----	-----	
msa237615.2{328_M781}	TVKSKQ	-----	-----	-----	-----	
msa237615.2{328_H36B}	TVKSKQ	-----	-----	-----	-----	
msa237615.2{328_JM9130013}	TVKSKQ	-----	-----	-----	-----	
msa237615.2{328_18RS21}	TVKSKQ	-----	-----	-----	-----	
msa237615.2{328_090}	TVKSKQ	-----	-----	-----	-----	
msa237615.2{328_CJB110}	TVKSKQ	-----	-----	-----	-----	
Consensus	*****	*****	*****	*****	*****	

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7201

STRAIN 2603

ATGAATAAACCGGTAAAAATCGTTGCAACACTTGGTCCGCGGTTGAATTCGGTGGTG
 GTAAGAAGTTTGGTGAGTCTGGATACCTGGGGTGAAGCCTTGACGTAGAAGCTTCAGCAG
 AAAAAATTGCTCAATTGATTAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCACATG
 GAGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAGAGATTGCAG
 GACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAATTCGTACAGAAGCTTTTG
 AAGATGGTGCAGATTTCCATTATATACACAGGTACAAAAATTACGTGTTGCTACTAAGC
 AAGGTATCAAATCACTCCAGAAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCT
 TTGATGACGTTGAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTG
 TGTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCCCTTA
 TTGGTAAACAAAAAGGTGTAACATCCCTTATATAAAATTCCTTTCCAGCACTTGCGAG
 AACCGGATAATGCTGATATCCGTTTGGACTTGAGCAAGGACTTAACCTTATTGCTATCT
 CATTTGTACGTACTGCTAAAGATGTTAATGAAGTTCGTGCTATTTTGAAGAACTGGsm
 ATGGACACGTTAAGTTGTTTCTAAATTTGAAATCAACAAGGTATCGATAATATTGATG
 AGATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCGAAGTTC
 CATTTGAAATGTTTCCAGTTTACCAAAAAATGATCATTAAGTTAATGCAGCTGGTA
 AAGCAGTTATTACAGCAACAAATATGCTTGAACAATGACTGATAAACCCAGTGCAGCTC
 GTTCAGAAGTATCTGATGCTTCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTT
 CAGGTGAGTCAGCTAATGGTAAATCCCAAGTTGAGTCAGTTGTAACAATGGCTACTATTG
 ATAAAAATGCTCAAACATTACTCAATGAGTATGGTGGCTTAGACTCATCTGCCATTCAC
 GTAATAACAAAACTGATGTTATTGCTATCTCGGTTAAAGATGCAACACACTCAATGGATA
 TCAAACTTGTGTTAACTACTGAAACAGGTAAATACAGCTCGTGCCATTCTTAAATTC
 GTCCAGATGCAACACTTTGGCTGTTACATTTGATGAAAAAGTACAACGTTCAATTGATGA
 TTAATCGGGTGTATCCCTGCTTGCAGACAAACAGCATCTACAGATGATATGTTTG
 AGGTTGCAGAAGCTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATAATATCGTTA
 TCGTTGACGGTGTTCGTAGGTACAGGTGGAACAAACAATGCGTGTTCGTACTGTTA
 AA

SEQ ID NO. 7202

STRAIN 090

AATAAACCGGTAAAAATCGTTGCAACACT
 TGGTCCGCGGTAGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTGGAT
 ACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCTCAA
 TTGATTAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCACATGGAGA
 TCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAGAGA
 TTGCAGGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAAT
 CGTACAGAATCTTTTGAAGATGGTTCAGATTTCCTATTATATACACAGG
 TACAGAATTACGTGTTGCTACTAAGCAAGGTATCAAATCACTCCAGAAG
 TGATTGCAATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAA
 GTTGGTAAAGCAATCCTTGTGATGATGGTAACTAGGTCTTACTGTGTT
 TGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATG
 GCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAATTCCT
 TTCCCAgCACTTGCAGAACCGGATAATGCTGATCCGTTTGGACTTGA
 GCAAGGACTTAACCTTTATTGCTATCTCATTGTGACGTACTGCTAAGATG
 TTAATGAAGTTCGTGCTATTGTTGAAGAACTGGCAATGACATGTTAAG
 TTGTTTGTCAAATTTGAAATCAACAAGGTATCGATAATATTGATGAGAT
 TATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCG
 AAGTTCCTATTGAAATGGTCCAGTTTACCAAAAAATGATCATTACTAAA
 GTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAATATGCTTGAAAC
 AATGACTGATAAACCCAGTGCAGCTCGTTGAGAAGTATCTGATGCTTCA
 ATGCTGTTATTGATGGTACTGATGCTACAATGCTTTAGGTGAGTCAGCT
 AATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGATAA
 AAATGCTCAAACATTACTCAATGAGTATGGTGGCTTAGACTCATCTGCAT
 TCCCACTAATAACAAAACTGATGTTATTGCTATCTGCGGTTAAAGATGCA
 ACACACTCAATGGATATCAAATTTGTTGTGACAATTACTGAAACAGGTAA
 TACAGCTCGTGCCATTCTAAATTCGTCAGATGCAGACATTTTGGCTG
 TTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACTGGGGTGT
 ATCCCTGTCTTGCAGACAAACAGCATCTACAGATGATATGTTTGAGGT
 TGCAGAAGCTGTAGCACTTGAAGCAGGACTTGTGAATCAGGCGATAATA
 TCGTTATCGTTGACGGTGTTCGTAGGTACAGGTGGAACAAACAATG
 CGTGTTCGTACTGTTAAA

SEQ ID NO. 7203

STRAIN A909

AATAAACCGGTAAAAATCGTTGCAACACTTGGTC
 CTGCGGTTGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTGGATCTGG
 GGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCTCAATTGAT
 TAAAGAAGGTGCTAACGTTTCCGTTTCAACTTCTCACATGGAGATCATG
 CTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAGAGATTGCA
 GGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAATTCGTAC
 AGAATCTTTTGAAGATGGTGCAGATTTCCTATTATATACACAGGTACAA
 AATTACGTTGTTGCTACTAAGCAAGGTATCAAATCACTCCAGAAGTGATT
 GCAATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAAGTTGG
 TAAGCAATCCTTGTGATGATGGTAACTAGGTCTTACTGTGTTTGCAA
 AAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCCTT
 ATTGGTAAACAAAAAGGTGTAACATCCCTTATATAAAATTCCTTTCC
 AGCACTTGCAGAACCGGATAATGCTGATATCCGTTTGGACTTGAGCAAG
 GACTTAACCTTTATTGCTATCTCATTGTACGTACTGCTAAAGATGTTAAT
 GAAGTTTCGTGCTATTGTTGAAGAACTGGCAATGGACAGCTTAAGTTGTT
 TGCTAAAAATTTGAAATCAACAAGGTATCGATAATATTGATGAGATTATCG
 AAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCGAAGTT
 CCATTGAAATGTTCCAGTTTACCAAAAAATGATCATTAAGTTAA

Table 72: Comparative Sequences relating to SAG0941

TGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGAAACAATGA
 CTGATAAACCCAGTGCAGACTCGTTTCAGAGATCTGATGTCTTCAATGCT
 GTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCAGCTAATGG
 TAAATACCCAGTTGAGTCAGTTCGTACCAATGGCTACTATTGATAAAAATG
 CTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTGCATTCCCA
 CGTAATAACAAAACCTGATGTTATTGCACTCGCGTTAAAGATGCAACACA
 CTCATGGATATCAAACTTGTGTAAACAATTACTGAAACAGGTAATACAG
 CTGTCGCCATTCTTAAATCCGTCCAGATGCAGACATTTTGGCTGTTACA
 TTTGATGAAAAAGTACAACGTTTCATTGATGATTAACCTGGGGTGTATCCC
 TGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGGAGTTGCAG
 AACGTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATAATATCGTT
 ATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACCAATGCGTGT
 TCGTACTGTTAAA

SEQ ID NO. 7204

STRAIN H36B

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTTGAATTCGGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTTCGTACAGAACTTTTGAAGATGGTGCAGATTTCCATTATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCAAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAGCAAGGACTTAACCTTTATTGCTATCTCATTGTGACGTACTGCTAAG
 ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGTCTAAAAATGAAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCAITACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACCAATGACTGATAAACCAAGTGCAGACTCGTTGAGAAGTATCTGATGTCT
 TCAATGCTGTTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAAATGGCTACTATTGA
 TAAAAATGCTCAAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCACGCTAATAACAAACTGATGTTATTGCACTCGCGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTCTTAAATCCGTCCAGATGCAGACATTTTGG
 CTGTTACATTGATGAAAAAGTACAACGTTTCATTGATGATTAACCTGGGGT
 GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTTGCAGAACGTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7205

STRAIN 18RS21

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTTGAATTCGGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGCAGATTTCCATTATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCAAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAGCAAGGACTTAACCTTTATTGCTATCTCATTGTGACGTACTGCTAAG
 ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGTCTAAAAATGAAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCAITACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACCAATGACTGATAAACCAAGTGCAGACTCGTTGAGAAGTATCTGATGTCT
 TCAATGCTGTTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCACGCTAATAACAAACTGATGTTATTGCACTCGCGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTCTTAAATCCGTCCAGATGCAGACATTTTGG
 CTGTTACATTGATGAAAAAGTACAACGTTTCATTGATGATTAACCTGGGGT
 GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTTGCAGAACGTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7206

Table 72: Comparative Sequences relating to SAG0941

STRAIN M732

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGAGATTCCATTATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCGAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACCTTTATGCTATCTCATTGTGACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGCTAAAAATTGAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAACTGACTGATAAACCCAGTGCAGTCTCGTTGAGATATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTGAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTACAAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAATGTTGTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTCAATGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTGA
 GGTTCAGAACCTGTAGCACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTCGTACTGTTAA

SEQ ID NO. 7207

STRAIN COH1

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGAGATTCCATTATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGTTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCGAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACCTTTATGCTATCTCATTGTGACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGCTAAAAATTGAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAACTGACTGATAAACCCAGTGCAGTCTCGTTGAGATATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTACAAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAATGTTGTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTCAATGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTGA
 GGTTCAGAACCTGTAGCACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTCGTACTGTTAA

SEQ ID NO. 7208

STRAIN M781

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGAGATTCCATTATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGTTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCGAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACCTTTATGCTATCTCATTGTGACGTACTGCTAAAG

Table 72: Comparative Sequences relating to SAG0941

ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGCTAAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCCAGTGGCAGTTCGTTCAGAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTGAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAGTTCGCTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGAGCACTTGAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTTATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7209

STRAIN CJB110

AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTTGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCGGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCTCTTGTATCTAAAGGACCTGAA
 ATTTCGTACAGAACTTTTGAAGATGGTGCAGATTTCATTCATATACAAC
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAACAAGGACTTAACCTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACAGTT
 AAGTTGTTTGTAAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCCAGTGGCAGTTCGTTCAGAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTGAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAATTCGCTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGAGCACTTGAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTATATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7210

STRAIN 1169NT

AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTGAAGTTCCGGTGGTGAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCGGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCTCTTGTATCTAAAGGACCTGAA
 ATTTCGTACAGAACTTTTGAAGATGGTGCAGATTTCATTCATATACAAC
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAGCAAGGACTTAACCTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACAGTT
 AAGTTGTTTGTAAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AaAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCCAGTGGCAGTTCGTTCAGAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTGAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAATTCGCTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGAGCACTTGAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTATATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAAA

Table 72: Comparative Sequences relating to SAG0941

ATATCGTTATCGTTGCAGGTGTTCTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAA

SEQ ID NO. 7211

STRAIN JM9130013

AATAAACCGGTAAAAATCGTTGCAAC

ACTTGGTCTCGCGGTAGAAATCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACCTGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTTCCTGTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCTGTAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCTCTCTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTGAAGATGGTTCAGATTTCCATTCATATACAAAC
AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAAATCCTTGTGATGATGGTAACTAGGTCTTACTGT
GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
CCTTTCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTGGACT
TGAGCAAGGACTTAACCTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTCTGCTATTGTTGTAAGAACTGGCAATGGACATGTT
AAGTTGTTTGTCTAAATTTGAATAACCAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAAGCTGGTAAAGCAGTTATACAGCAACAAATATGCTTGA
AACAACTGACTGATAAACCCAGTGCAGCTCGTTTCAAGATATCTGATGCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCACTTCTGTAATGGCTACTATTGA
TAAAAATGCTCAAACTATTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
CATTTCCAGCTAATAACAAAACTGATGTTATGCACTCTGCGGTTAAAGAT
GCAACCACTCAATGGATATCAAACTGTTTGTGACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATCCGTCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACTGTTTATTGATGATTAACTGGGT
GTTATCCCTGTCTTGCAGACAAACAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAGcACTTGAAGCAGGACTTGTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAA

PRETTY of: /biotmp/msa277466.2{*} February 24, 2003 01:44 ..

	1		50
msa277466.2{330_090}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_JM9130013}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_18RS21}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_2603}	atgAATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_A909}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_H36B}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_CJB110}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_COH1}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_M732}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_1169NT}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_M781}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
Consensus	*****	*****	*****
	51		100
msa277466.2{330_090}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_JM9130013}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_18RS21}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_2603}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_A909}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_H36B}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_CJB110}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_COH1}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_M732}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_1169NT}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_M781}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
Consensus	*****	*****	*****
	101		150
msa277466.2{330_090}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_JM9130013}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_18RS21}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_2603}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_A909}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_H36B}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_CJB110}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_COH1}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_M732}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_1169NT}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_M781}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
Consensus	*****	*****	*****
	151		200
msa277466.2{330_090}	AACGTTTTTC	GTTTCAACTT	CTCACATGGA

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_JM9130013}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_18RS21}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_2603}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_A909}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_H36B}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_CJB110}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_COH1}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_M732}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_1169NT}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_M781}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_JM9130013}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_18RS21}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_2603}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_A909}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_H36B}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_CJB110}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_COH1}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_M732}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_1169NT}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_M781}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_JM9130013}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_18RS21}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_2603}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_A909}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_H36B}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_CJB110}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_COH1}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_M732}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_1169NT}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_M781}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	GATGGTtCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_JM9130013}	GATGGTtCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_18RS21}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_2603}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_A909}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_H36B}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_CJB110}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_COH1}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_M732}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_1169NT}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_M781}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
Consensus	*****_***	*****	*****	*****_***	*****
msa277466.2{330_090}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_JM9130013}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_18RS21}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_2603}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_A909}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_H36B}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_CJB110}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_COH1}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_M732}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_1169NT}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_M781}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_JM9130013}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_18RS21}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_2603}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_A909}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_H36B}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_CJB110}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_COH1}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_M732}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_1169NT}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_M781}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
Consensus	*****	*****	*****	*****	*****

451

500

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_090}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_JM9130013}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_18RS21}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_2603}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_A909}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_H36B}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_CJB110}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_COH1}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_M732}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_1169NT}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_M781}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_JM9130013}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_18RS21}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_2603}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_A909}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_H36B}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_CJB110}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_COH1}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_M732}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_1169NT}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_M781}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACG	ACTTGCAGAA
msa277466.2{330_JM9130013}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACG	ACTTGCAGAA
msa277466.2{330_18RS21}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACG	ACTTGCAGAA
msa277466.2{330_2603}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACG	ACTTGCAGAA
msa277466.2{330_A909}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACG	ACTTGCAGAA
msa277466.2{330_H36B}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACG	ACTTGCAGAA
msa277466.2{330_CJB110}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACG	ACTTGCAGAA
msa277466.2{330_COH1}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACG	ACTTGCAGAA
msa277466.2{330_M732}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACG	ACTTGCAGAA
msa277466.2{330_1169NT}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACG	ACTTGCAGAA
msa277466.2{330_M781}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACG	ACTTGCAGAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_JM9130013}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_18RS21}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_2603}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_A909}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_H36B}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_CJB110}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_COH1}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_M732}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_1169NT}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_M781}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTGTGCTA
msa277466.2{330_JM9130013}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTGTGCTA
msa277466.2{330_18RS21}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTGTGCTA
msa277466.2{330_2603}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTGTGCTA
msa277466.2{330_A909}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTGTGCTA
msa277466.2{330_H36B}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTGTGCTA
msa277466.2{330_CJB110}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTGTGCTA
msa277466.2{330_COH1}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTGTGCTA
msa277466.2{330_M732}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTGTGCTA
msa277466.2{330_1169NT}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTGTGCTA
msa277466.2{330_M781}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTGTGCTA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TTTGTGAAGA	AACCTGGcaAT	GGACATGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_JM9130013}	TTTGTGAAGA	AACCTGGcaAT	GGACATGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_18RS21}	TTTGTGAAGA	AACCTGGcaAT	GGACATGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_2603}	TTTGTGAAGA	AACCTGGsmAT	GGACATGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_A909}	TTTGTGAAGA	AACCTGGcaAT	GGACATGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_H36B}	TTTGTGAAGA	AACCTGGcaAT	GGACATGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_CJB110}	TTTGTGAAGA	AACCTGGcaAT	GGACATGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_COH1}	TTTGTGAAGA	AACCTGGcaAT	GGACATGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_M732}	TTTGTGAAGA	AACCTGGcaAT	GGACATGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_1169NT}	TTTGTGAAGA	AACCTGGcaAT	GGACATGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_M781}	TTTGTGAAGA	AACCTGGcaAT	GGACATGTTA	AGTTGTTTGC	TAAAATTGAA
Consensus	*****	*****	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941

		751					800
msa277466.2{330_090}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_JM9130013}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_18RS21}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_2603}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_A909}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_H36B}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_CJB110}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_COH1}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_M732}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_1169NT}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_M781}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
Consensus	*****	*****	*****	*****	*****		
		801					850
msa277466.2{330_090}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_JM9130013}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_18RS21}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_2603}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_A909}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_H36B}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_CJB110}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_COH1}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_M732}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_1169NT}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_M781}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
Consensus	*****	*****	*****	*****	*****		
		851					900
msa277466.2{330_090}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_JM9130013}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_18RS21}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_2603}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_A909}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_H36B}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_CJB110}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_COH1}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_M732}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_1169NT}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_M781}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
Consensus	*****	*****	*****	*****	*****		
		901					950
msa277466.2{330_090}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_JM9130013}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_18RS21}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_2603}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_A909}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_H36B}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_CJB110}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_COH1}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_M732}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_1169NT}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_M781}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
Consensus	*****	*****	*****	*****	*****		
		951					1000
msa277466.2{330_090}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_JM9130013}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_18RS21}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_2603}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_A909}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_H36B}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_CJB110}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_COH1}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_M732}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_1169NT}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_M781}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
Consensus	*****	*****	*****	*****	*****		
		1001					1050
msa277466.2{330_090}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_JM9130013}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_18RS21}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_2603}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_A909}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_H36B}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_CJB110}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_COH1}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_M732}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_1169NT}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_M781}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
Consensus	*****	*****	*****	*****	*****		

Table 72: Comparative Sequences relating to SAG0941

		1051			1100
msa277466.2{330_090}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_JM9130013}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_18RS21}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_2603}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_A909}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_H36B}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_CJB110}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_COH1}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_M732}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_1169NT}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_M781}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
Consensus		*****	*****	*****	*****
		1101			1150
msa277466.2{330_090}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_JM9130013}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_18RS21}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_2603}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_A909}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_H36B}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_CJB110}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_COH1}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_M732}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_1169NT}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_M781}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
Consensus		*****	*****	*****	*****
		1151			1200
msa277466.2{330_090}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_JM9130013}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_18RS21}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_2603}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_A909}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_H36B}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_CJB110}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_COH1}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_M732}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_1169NT}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_M781}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
Consensus		*****	*****	*****	*****
		1201			1250
msa277466.2{330_090}		AAACTTGTG	TgACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_JM9130013}		AAACTTGTG	TgACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_18RS21}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_2603}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_A909}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_H36B}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_CJB110}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_COH1}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_M732}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_1169NT}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_M781}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
Consensus		*****	*****	*****	*****
		1251			1300
msa277466.2{330_090}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_JM9130013}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_18RS21}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_2603}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_A909}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_H36B}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_CJB110}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_COH1}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_M732}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_1169NT}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_M781}		TAAgTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
Consensus		***-*****	*****	*****	*****
		1301			1350
msa277466.2{330_090}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_JM9130013}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_18RS21}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_2603}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_A909}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_H36B}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_CJB110}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_COH1}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_M732}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_1169NT}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_M781}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT

Table 72: Comparative Sequences relating to SAG0941

Consensus	*****	*****	*****	*****	*****
	1351				1400
msa277466.2{330_090}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_JM9130013}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_18RS21}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_2603}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_A909}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_H36B}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_CJB110}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_COH1}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_M732}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_1169NT}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_M781}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
Consensus	*****	*****	*****	*****	*****
	1401				1450
msa277466.2{330_090}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_JM9130013}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_18RS21}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_2603}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_A909}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_H36B}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_CJB110}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_COH1}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_M732}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_1169NT}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_M781}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
Consensus	*****	*****	*****	*****	*****
	1451				1500
msa277466.2{330_090}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_JM9130013}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_18RS21}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_2603}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_A909}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_H36B}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_CJB110}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_COH1}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_M732}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_1169NT}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_M781}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 7212

STRAIN 2603 frame: 1

MNKRKIVATLGPVAFVFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHG
 DHAEQGMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGTCLRVATKQ
 GIKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVENDGLI
 GKQGVNIPTTKIPFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGX
 GHVKLFAKIEHQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGK
 AVITATNMLETMDTKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATID
 KNAQTLLNEYGRDLSSAFPRNKTVDIASAVKDATHSMDIKLVVTTITETGNTARAIKFRP
 PDADILAVTFDEKVRQSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIIV
 VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7213

STRAIN 090 frame: 1

NKRKIVATLGPVAFVFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGTCLRVATKQ
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVENDGLI
 GKQGVNIPTTKIPFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGX
 GHVKLFAKIEHQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGK
 VITATNMLETMDTKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATID
 NAQTLLNEYGRDLSSAFPRNKTVDIASAVKDATHSMDIKLVVTTITETGNTARAIKFRP
 DADILAVTFDEKVRQSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIIV
 VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7214

STRAIN A909 frame: 1

NKRKIVATLGPVAFVFRGGKKFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
 HAEQGMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGTCLRVATKQ
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVENDGLI
 GKQGVNIPTTKIPFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGX
 GHVKLFAKIEHQGIDNIDEIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGK
 VITATNMLETMDTKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATID
 NAQTLLNEYGRDLSSAFPRNKTVDIASAVKDATHSMDIKLVVTTITETGNTARAIKFRP
 DADILAVTFDEKVRQSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIIV
 VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7215

STRAIN H36B frame: 1

Table 72: Comparative Sequences relating to SAG0941

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIEHQQIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7216

STRAIN 18RS21 frame: 1

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIEHQQIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7217

STRAIN M732 frame: 1

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIEHQQIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7218

STRAIN COH1 frame: 1

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIEHQQIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7219

STRAIN M781 frame: 1

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIEHQQIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7220

STRAIN CJB110 frame: 1

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIEHQQIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7221

STRAIN 1169NT frame: 1

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIEHQQIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
AGVPVGTGGTNTMRVRTVK

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7222

STRAIN JM9130013 frame: 1

NKRVKIVATLGPVAFRGGKFGESGYWGESLDVEASAEKIAQLIKEGANVFRNFHSHG
 HAEQGARMATVRKAEIAGQKVGFLDITKGPETELFEDGSDHFSYTTCTKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVENDGLIG
 KQKGVNIPYTKIPFPALAEADNADIRFGLGGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFKAIENQOQIDNIDEIIEAADGIMIAARGDMGIEVFPFEMVVPYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVTRMATIDK
 NAQTLLENYGRLLDSSAFPRNKTVDVIAAVKDATHSMDIKLVVTTITETGTARAIKFRP
 DADILAVTFDEKVRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIIVIV
 AGVPVGTGGTNTMRVRTVK

PRETTY of: /biotmp/msa277662.2{*} February 24, 2003 01:49 ..

msa277662.2{330_18RS21}	1	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	50
msa277662.2{330_A909}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_CJB110}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_H36B}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_1169NT}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_COH1}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_M732}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_M781}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_JM9130013}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_090}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_2603}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
Consensus		*****	*****	*****	*****	*****	
msa277662.2{330_18RS21}	51	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	100
msa277662.2{330_A909}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_CJB110}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_H36B}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_1169NT}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_COH1}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_M732}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_M781}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_JM9130013}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_090}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_2603}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
Consensus		*****	*****	*****	*****	*****	
msa277662.2{330_18RS21}	101	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	150
msa277662.2{330_A909}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_CJB110}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_H36B}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_1169NT}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_COH1}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_M732}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_M781}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_JM9130013}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_090}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_2603}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
Consensus		** -*****	** -*****	*****	*****	*****	
msa277662.2{330_18RS21}	151	VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	200
msa277662.2{330_A909}		VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_CJB110}		VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_H36B}		VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_1169NT}		VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_COH1}		VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_M732}		VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_M781}		VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_JM9130013}		VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_090}		VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_2603}		VDDGKLGTLV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
Consensus		*****	*****	*****	*****	*****	
msa277662.2{330_18RS21}	201	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	250
msa277662.2{330_A909}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_CJB110}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_H36B}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_1169NT}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_COH1}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_M732}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_M781}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_JM9130013}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_090}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_2603}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGx	GHVKLFKAKIE	
Consensus		*****	*****	*****	*****	*****	

Table 72: Comparative Sequences relating to SAG0941

	251				300
msa277662.2{330_18RS21}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_A909}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_CJB110}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_H36B}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_1169NT}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_COH1}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_M732}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_M781}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_JM9130013}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_090}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_2603}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
Consensus	*****	*****	*****	*****	*****
	301				350
msa277662.2{330_18RS21}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_A909}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_CJB110}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_H36B}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_1169NT}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_COH1}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_M732}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_M781}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_JM9130013}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_090}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_2603}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
Consensus	*****	*****	*****	*****	*****
	351				400
msa277662.2{330_18RS21}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_A909}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_CJB110}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_H36B}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_1169NT}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_COH1}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_M732}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_M781}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_JM9130013}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_090}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
msa277662.2{330_2603}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAA	VKDATHSMDI
Consensus	*****	*****	*****	*****	*****
	401				450
msa277662.2{330_18RS21}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_A909}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_CJB110}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_H36B}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_1169NT}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_COH1}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_M732}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_M781}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_JM9130013}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_090}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_2603}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
Consensus	*****	*****	*****	*****	*****
	451				500
msa277662.2{330_18RS21}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_A909}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_CJB110}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_H36B}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_1169NT}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_COH1}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_M732}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_M781}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_JM9130013}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_090}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_2603}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
Consensus	*****	*****	*****	*****	*****

Table 73: Comparative Sequences relating to SAG0981

SEQ ID NO. 7301

STRAIN 2603

TTGCTCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTTAGCATTAAATCGGTGAT
 ATCATTAAATCAAACAGATACCTGAAACGTGAAACCTTCCAAACAGTCTTTTCAGCAACTA
 ATGACCGAACTATCTGATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCT
 GGTGATGAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCAT
 ATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTACAGGAAACATTATA
 ACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCTGCCTACTGGCATGCTCGC
 TCAGCTATTAAATCATATACATGATAAAATGATTATGGAACAGTTCAAGTAGCTATTGTC
 CTTGATGATGAAGACCAAAACCTTGAATTAACACTAAATAGTCTCATTTACAGCTGGTGAT
 TTTATCAAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAA
 GATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGGAAAATATTGAACCT
 AGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTGAAGATTACTTAAGAACGAGAACA
 CAGGCAGCCGATCTATTAGTTAAAGTTGCACCTCAAACTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7302

STRAIN 090

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTT
 AGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTGAAACGTGAAA
 CTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAACTATCTGATGTATAT
 GGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTTCA
 AGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCATATTTC
 AACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTACAGGAAAC
 ATTATAACATCCATCAATTTAAATGAAAGTATCGGTGCTGATGGTCTGCTG
 CTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAAAATGATT
 ATGGAACAGTTTCAAGTAGCTATTGCTTGGATGATGAAGACCAAAACCTT
 GAATTAACACTAAATAGTCTCATTTACAGCTGGTGATTTTATCAAGTCAAA
 ATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGATA
 ATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGGAAAATATT
 GAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTGAAGATTTA
 CTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCACCTC
 AAATAAGGGGAAGCTATGATTTC

SEQ ID NO. 7303

STRAIN A909

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTAT
 TTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTGAAACGTGA
 AACTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAACTATCTGATGTAT
 ATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTT
 CAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCATAT
 TCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTACAGGAA
 ACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGATGGTCTC
 GCCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAAAATGA
 TTATGGAACAGTTCAAGTAGCTATTGCTTGGATGATGAAGACCAAAACC
 TTGAATTAAACACTAAATAGTCTCATTTACAGCTGGTGATTTTATCAAGTCA
 AAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGA
 TAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGGAAAATA
 TTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTGAAGATT
 TACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCAC
 TCAAACTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7304

STRAIN H36B

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTTGA
 ACGTGAACCTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGA
 CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTA
 CAGGAACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTGCTTGGATGATGAAGACC
 AAAACCTTGAATTAAACACTAAATAGTCTCATTTACAGCTGGTGATTTTATC
 AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7305

STRAIN 18RS21

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTTGA
 ACGTGAACCTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGA
 CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTA
 CAGGAACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTGCTTGGATGATGAAGACC
 AAAACCTTGAATTAAACACTAAATAGTCTCATTTACAGCTGGTGATTTTATC
 AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACTAAAGGGGAAGCTATGATTTC

Table 73: Comparative Sequences relating to SAG0981

TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACATAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7306

STRAIN M732

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTG
 AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
 GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 TGAATTTCAAGCTTTATTTGAACCAATCAAAAAAGGTATTTCAAATTTATTG
 ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGT
 ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
 TGGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
 CAAAACCTTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTAT
 CAAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATAC
 TTCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTG
 GAAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAGCAAGCGGTCT
 GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 GTTGCACTCAAACATAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7307

STRAIN COH1

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTG
 AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
 GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 TGAATTTCAAGCTTTATTTGAACCAATCAAAAAAGGTATTTCAAATTTATTG
 ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGT
 ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
 TGGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
 CAAAACCTTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTAT
 CAAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATAC
 TTCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTG
 GAAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAGCAAGCGGTCT
 GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 GTTGCACTCAAACATAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7308

STRAIN M781

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTTGAACCAATCAAAAAAGGTATTTCAAATTTATTGA
 CCAATTTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTGA
 CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AATGATTATGGAACAGTTCAAGTAGCTATTTGCCITGATGATGAAGACC
 AAAACCTTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
 AAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACATAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7309

STRAIN CJB110

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TTTATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACT
 TGAACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTAT
 CTGATGTATATGGTGAAGAGCTGATTTCTCTATTCACTATTACAGCTGGT
 GATGAATTTCAAGCTTTATTTGAACCAATCAAAAAAGGTATTTCAAATTTAT
 TGACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCG
 GTACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCT
 GATGGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 TAAAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCITGATGATGAAG
 ACCAAAACCTTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTT
 ATCAAGTCAAAATGGACTACTAACCAATTTCAAATGCTTGAGCACTTAAT
 ACTTCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACT
 TGGAAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAGCAAGCGGT
 CTGAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAA
 AAGTTGCACTCAAACATAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7310

STRAIN JM9130013

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG

Table 73: Comparative Sequences relating to SAG0981

ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT GAATTTCAAGCTTTATGAAACCATCAAAAAAGGTATTTCAAATTATTGA CCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTTCCGGCTCGGTA CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT GGTCTGCTACTGGCATGCTCGCTCAGCTATTATCATATACATGATAA AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC AAAACCTTGAATTAACTAACTAAATAGTCTCATTTCAGCTGGTGATTTTATC AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCACTGG AAAAATATTGAACCTAGTGGCTGACTAAACGCCTTAAGCAAGCGGTCTG AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG TTGCACTCAAATAAAGGGGAAGCTATGATTTTC									
PRETTY of: /biotmp/msa31912.2{*} February 18, 2003 08:19 ..									
1 50									
msa31912.2{338_18RS21}	---	TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT			
msa31912.2{338_2603}	ttg	TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT			
msa31912.2{338_A909}	---	TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT			
msa31912.2{338_H36B}	---	TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT			
msa31912.2{338_JM9130013}	---	TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT			
msa31912.2{338_COH1}	---	TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT			
msa31912.2{338_M732}	---	TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT			
msa31912.2{338_M781}	---	TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT			
msa31912.2{338_090}	---	TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT			
msa31912.2{338_CJB110}	---	TCTGCTA	TAATAGACAA	AAAGGTGGTG	gTATTTATGT	ATTAGCATT			
Consensus	*****	*****	*****	*****	*****	*****			
51 100									
msa31912.2{338_18RS21}	AAT	CGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC			
msa31912.2{338_2603}	AAT	CGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC			
msa31912.2{338_A909}	AAT	CGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC			
msa31912.2{338_H36B}	AAT	CGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC			
msa31912.2{338_JM9130013}	AAT	CGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC			
msa31912.2{338_COH1}	AAT	CGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC			
msa31912.2{338_M732}	AAT	CGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC			
msa31912.2{338_M781}	AAT	CGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC			
msa31912.2{338_090}	AAT	CGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC			
msa31912.2{338_CJB110}	AAT	CGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC			
Consensus	*****	*****	*****	*****	*****	*****			
101 150									
msa31912.2{338_18RS21}	AAC	AGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA			
msa31912.2{338_2603}	AAC	AGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA			
msa31912.2{338_A909}	AAC	AGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA			
msa31912.2{338_H36B}	AAC	AGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA			
msa31912.2{338_JM9130013}	AAC	AGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA			
msa31912.2{338_COH1}	AAC	AGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA			
msa31912.2{338_M732}	AAC	AGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA			
msa31912.2{338_M781}	AAC	AGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA			
msa31912.2{338_090}	AAC	AGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA			
msa31912.2{338_CJB110}	AAC	AGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA			
Consensus	*****	*****	*****	*****	*****	*****			
151 200									
msa31912.2{338_18RS21}	GAG	CTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT			
msa31912.2{338_2603}	GAG	CTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT			
msa31912.2{338_A909}	GAG	CTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT			
msa31912.2{338_H36B}	GAG	CTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT			
msa31912.2{338_JM9130013}	GAG	CTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT			
msa31912.2{338_COH1}	GAG	CTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT			
msa31912.2{338_M732}	GAG	CTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT			
msa31912.2{338_M781}	GAG	CTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT			
msa31912.2{338_090}	GAG	CTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT			
msa31912.2{338_CJB110}	GAG	CTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT			
Consensus	*****	*****	*****	*****	*****	*****			
201 250									
msa31912.2{338_18RS21}	ATT	GAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG			
msa31912.2{338_2603}	ATT	GAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG			
msa31912.2{338_A909}	ATT	GAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG			
msa31912.2{338_H36B}	ATT	GAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG			
msa31912.2{338_JM9130013}	ATT	GAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG			
msa31912.2{338_COH1}	ATT	GAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG			
msa31912.2{338_M732}	ATT	GAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG			
msa31912.2{338_M781}	ATT	GAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG			
msa31912.2{338_090}	ATT	GAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG			
msa31912.2{338_CJB110}	ATT	GAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG			
Consensus	*****	*****	*****	*****	*****	*****			
251 300									
msa31912.2{338_18RS21}	CTC	TAAACCC	TGTTAATGTA	AGGTTCCGCC	TCGGTACAGG	AAACATTATA			
msa31912.2{338_2603}	CTC	TAAACCC	TGTTAATGTA	AGGTTCCGCC	TCGGTACAGG	AAACATTATA			

Table 73: Comparative Sequences relating to SAG0981

msa31912.2{338_A909}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_H36B}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_JM9130013}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_COH1}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_M732}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_M781}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_090}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_CJB110}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	301	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	350	CTGCCTACTG
msa31912.2{338_2603}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_A909}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_H36B}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_JM9130013}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_COH1}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_M732}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_M781}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_090}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_CJB110}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
Consensus	*****	***-*****	*****	*****	*****		
msa31912.2{338_18RS21}	351	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	400	GATTATGGAA
msa31912.2{338_2603}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_A909}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_H36B}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_JM9130013}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_COH1}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_M732}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_M781}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_090}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_CJB110}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	401	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	450	CCTTGAATTA
msa31912.2{338_2603}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_A909}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_H36B}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_JM9130013}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_COH1}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_M732}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_M781}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_090}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_CJB110}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	451	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	500	CAAAATGGAC
msa31912.2{338_2603}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_A909}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_H36B}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_JM9130013}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_COH1}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_M732}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_M781}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_090}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_CJB110}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	501	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	550	GATAAATTATC
msa31912.2{338_2603}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_A909}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_H36B}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_JM9130013}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_COH1}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_M732}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_M781}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_090}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_CJB110}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
Consensus	***-*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	551	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTGGAAAA	600	TATTGAACCT
msa31912.2{338_2603}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTGGAAAA	TATTGAACCT		
msa31912.2{338_A909}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTGGAAAA	TATTGAACCT		
msa31912.2{338_H36B}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTGGAAAA	TATTGAACCT		
msa31912.2{338_JM9130013}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTGGAAAA	TATTGAACCT		
msa31912.2{338_COH1}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTGGAAAA	TATTGAACCT		
msa31912.2{338_M732}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTGGAAAA	TATTGAACCT		

Table 73: Comparative Sequences relating to SAG0981

msa31912.2{338_M781}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_090}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_CJB110}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_2603}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_A909}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_H36B}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_JM9130013}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_COH1}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_M732}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_M781}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_090}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_CJB110}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_2603}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_A909}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_H36B}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_JM9130013}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_COH1}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_M732}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_M781}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_090}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_CJB110}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_2603}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_A909}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_H36B}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_JM9130013}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_COH1}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_M732}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_M781}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_090}	AAGGGGGAAG	CTATGATTTC			
msa31912.2{338_CJB110}	AAGGGGGAAG	CTATGATTTC			
Consensus	*****	*****			

SEQ ID NO. 7311

STRAIN 2603 frame: 1

LSAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFTTITA
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLTGNIITSINSNESIGADGPAYWHAR
 SAINHIHDKNDYGTQVVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQ
 DNYQEQFQHQLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7312

STRAIN 090 frame: 1

SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFTTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLTGNIITSINLNSIGADGPAYWHARS
 AINHIHDKNDYGTQVVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQFQHQLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7313

STRAIN A909 frame: 1

SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFTTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQFQHQLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7314

STRAIN H36B frame: 1

SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFTTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQFQHQLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7315

STRAIN 18RS21 frame: 1

SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFTTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQFQHQLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7316

STRAIN M732 frame: 1

SAIDKKVVFMYLALIGDIINSKQILERETFQQS FQQLMTELSDVYGEELISPFTTITAG

Table 73: Comparative Sequences relating to SAG0981

DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCQTQTGGGSYDF

SEQ ID NO. 7317

STRAIN COH1 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERET FQQSFQQLMTELSDVYGEELISPFITITAG
 DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCQTQTGGGSYDF

SEQ ID NO. 7318

STRAIN M781 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERET FQQSFQQLMTELSDVYGEELISPFITITAG
 DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCQTQTGGGSYDF

SEQ ID NO. 7319

STRAIN CJB110 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERET FQQSFQQLMTELSDVYGEELISLFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCQTQTGGGSYDF

SEQ ID NO. 7320

STRAIN JM9130013 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERET FQQSFQQLMTELSDVYGEELISPFITITAG
 DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCQTQTGGGSYDF

PRETTY of: /biotmp/msa32053.2{*} February 18, 2003 08:25 ..

	1		50
msa32053.2{338_18RS21}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_2603}	1SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_A909}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_CJB110}	~SAIIDKKVV	vFMYLALIGD	I INSKQILER
msa32053.2{338_COH1}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_H36B}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_JM9130013}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_M732}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_M781}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_090}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
Consensus	*****	-*****	*****

	51		100
msa32053.2{338_18RS21}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_2603}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_A909}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_CJB110}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_COH1}	ELISpFTITA	GDEFQALLKq	SKKVFQIIDH
msa32053.2{338_H36B}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_JM9130013}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_M732}	ELISpFTITA	GDEFQALLKq	SKKVFQIIDH
msa32053.2{338_M781}	ELISpFTITA	GDEFQALLKq	SKKVFQIIDH
msa32053.2{338_090}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
Consensus	****-****	*****	*****

	101		150
msa32053.2{338_18RS21}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_2603}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_A909}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_CJB110}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_COH1}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_H36B}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_JM9130013}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_M732}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_M781}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_090}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
Consensus	****-****	*****	*****

	151		200
msa32053.2{338_18RS21}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_2603}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_A909}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_CJB110}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_COH1}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_H36B}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_JM9130013}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_M732}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_M781}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ
Consensus	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ

Table 73: Comparative Sequences relating to SAG0981

msa32053.2{338_090}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ	DNYQEQFQHQ	KLAQLENIEP
Consensus	*****	*****	*****	*****	*****
	201			240	
msa32053.2{338_18RS21}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_2603}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_A909}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_CJB110}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_COH1}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_H36B}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_JM9130013}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_M732}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_M781}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_090}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
Consensus	*****	*****	*****	*****	

Table 74: Comparative Sequences relating to SAG1572

SEQ ID NO. 7401

STRAIN 2603

ATGGAAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTCTAT
CTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGGATTTTA
AGAGAAGTTGATTTTATTGTGTCAGAGGATACACGAAATACGGGACTTTTACTCAAGCAC
TTTGATATTACTACTAAACAAATTAGTTTTCACGAAACAAATGCTTACGATAAAATCTCT
GGGTTAATTGATTTGTTAAAAGAAGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATG
CCCTCTATTTCGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGTTTAGCT
CCACAACCTCATATTTTATTGGCTTCTTACCTCGTAAGAAAGGTCAACAAATAACTTTC
TTTGAACAAAGCAAGATTACCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTC
TCTGATACGCTAAACACATGAAAGAGATTTCGGGAGATCGCCAAGTTGTTTTAGTACGC
GAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCAATTAGTCAACTTTTAGAGCAT
ATTGAAAGGTTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAAGAGATAC
GAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTATTAGTAAAGAATATATCGCT
AATGGTGATAAACTAATCAAGCGATAAAAAAGTAGCAAGAATTTAATCTCAATAGA
CAAGAACTCTATGCTAGTTTCCATGATTTA

SEQ ID NO. 7402

STRAIN 090

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTACGGGACACT
CTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTG
CCATTAGGATTTTAAGAGAAGTTGATTTTATTGTGTCAGAGGATACACGA
AATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAG
TTTTACGAAACAAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGT
TAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCT
ATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGAT
CCCGTCTGTATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCG
CTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACCGCGT
AAGAAAGGTCAACAAATACTTTTGTAAACAAAGAAAGATTACCCCTGA
AACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAAC
ACATGAAGAGATTACGGAGATCGCCAAGTTGTTTAGTACGCGAATTG
ACGAACTCTATGAAGAGTATCAAAGAGGAACCAATTAGTCAACTTTTAGG
GCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATG
GTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTA
GTATTAGTAA

SEQ ID NO. 7403

STRAIN A909

AGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTCTATCTAG
TCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGG
ATTTAAGAGAAGTTGATTTTATTGTGTCAGAGGATACACGAAATACGGG
ACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGTTTTCAGC
AACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTTAAAGAA
GGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTCTGA
CCCGAGCATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCAAGTTG
TATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGG
TTAGCTCCACAACCTCATATTTTATGGCTTCTTACCACGTAAGAAAGG
TCAACAAATAACTTTCTTTGAACAAAGCAAGATTACCCCTGAAACACAAA
TCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAACACATGAAA
GAGATTACCGAGATCGCCAAGTTGTTTAGTACGCGAATTGACGAAACT
CTATGAAGAGTATCAAAGAGGAACCAATTAGTCAACTTTTAGAGCATATTG
AAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAAGAGA
GATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTATTAGT
AA

SEQ ID NO. 7404

STRAIN H36B

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATT
ACGGGACACTCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTGTGTCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTTA
ATTGATTGTGTTAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGG
AATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCCGTCTATCTATACCAAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTT
CTTACCGGTAAAGCAAGGTCAACAAATAACTTTTGTAAACAAAGAAAG
ATTACCCCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTCTCTGAT
ACGCTAAACACATGAAAGAGATTATGGAGATCGCCAAGTTGTTTAGT
ACCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACCAATTAGT
AACTTTTAGGGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAAGAGATACCTGAGCGAGTGAAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7405

STRAIN 18RS21

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATT
ACGGAACACTCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTGTGTCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTA
ATTGATTGTGTTAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGG

Table 74: Comparative Sequences relating to SAG1572

AATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCCAAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTTGTCTCCACACCTCATATTTTTATGGCTT
CTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAG
ATTACCCCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTCTCTGAT
ACGCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTGTTTAGT
ACGCCAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTC
AACTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7406

STRAIN M732

GAAATGCAAGTTCAAAAAAGTTTAAATCAAAT
ATACATTACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGA
TGATATGACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTT
GTGAGAGGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATT
ACTACTAAACAAATTAGTTTTCACGAACCAATGCTTACGATAAAATCTC
TGGGTTAATTGATTTGTAAAGAAGGGAATCTTTAGCCCAAGTATCTG
ATGACGGAATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCT
GCTATTGAAGGGGATATCCCAAGTTGTATCTATACCAGGAGCTAGCGCTGG
TATTACTGCTCTCATCGCTTCAGGTTTAGCTCCCAACCTCATATTTTTT
ATGGCTTCTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACA
AAGCAAGATTACCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGT
CTCTGATACGCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTG
TTTTAGTACGCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACC
ATTAGTCAACTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATG
CTTAATTATGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTA
GCCAACAAGATCCACTAGTATTAGTAA

SEQ ID NO. 7407

STRAIN COH1

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATATACATTAC
GGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGAC
TTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGAGAGG
ATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAA
CAAAATAGTTTTCACGAACCAATGCTTACGATAAAATCTCTGGGTTAAT
TGATTTGTGTAAGAAGAGGGAATCTTTAGCCCAAGTATCTGATGACAGGAA
TGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAA
GGGATATCCCAAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGC
TCTCATCGCTTCAGGTTTAGCTCCCAACCTCATATTTTTTATGGCTTCT
TACCAGTTAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGAT
TACCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATAC
GCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTGTTTATGATC
GCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAA
CTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTAT
TGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAG
ATCCACTAGTATTAGTAA

SEQ ID NO. 7408

STRAIN M781

AAATGCAAGTTCAAAAAAGTTTAAATCAAATATACATTACGGAACACTC
TATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGC
CATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGACAGGATACACGAA
ATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATAGT
TTTCACGAACCAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTT
AAAAAGAGGGAATCTTTAGCCCAAGTATCTGATGACGGAATGCCCTCTA
TTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATC
CCAGTTGTATCTATACAGGAGCTAGCGCTGGTATTACTGCTCTCATCGC
TTCAGGTTTAGCTCCCAACCTCATATTTTTTATGGCTTCTTACCAGTA
AGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGATTACCTGAA
ACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAACAC
CATGAAAGAGATTACGGAGATCGCCAAGTTGTTTATGACGGAATTGA
CGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAG
CATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGG
TAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAG
TATTAGTAA

A

SEQ ID NO. 7409

STRAIN CJB110

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACATTACGGGACAC
TCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGT
GCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGACAGGATACACG
AAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTA
GTTTTACGAACCAATGCTTACGATAAAATCTCTGGGTTAATTGATTTG
TTAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGACGGAATGCCCTC
TATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGA
TCCCGGTGCTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATC
GCTTCAGGTTTAGCTCCCAACCTCATATTTTTTATGGCTTCTTACCAGG
TAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGAAAGATTACCTG
AAACCAAAATCTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAAC
CATGAAAGAGATTACGGAGATCGCCAAGTTGTTTATGACGCGAATT

Table 74: Comparative Sequences relating to SAG1572

GACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAG
GGCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGAT
GGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAGATCCACT
AGTATTAGTAA

SEQ ID NO. 7410

STRAIN 1169NT

TGCAAGTTCAAAAAAGTTTAAATCAAATACACATTATGGGACACTCTAT
CTAGTCCCACTCCAATTGGTAATCTAGATGATGACTTTTCGTGCCAT
TAGGATTTTAAGAGAGTTGaTTTATTGTGTCAGAGGATACAGAAATA
CGGCACITTTACTCAAGCAGCTTTGATaTTACTACTAAACAAATTAGTTT
cACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTtGTTAAA
AGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATT
CTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTC
AGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACCACGTAAGA
AAGGTCAACAATAACTTTTGTGAAACAAGCAAGATTATCTGAAACA
CAAATCTTTTATGAGTACCGGtTTGAGTCTCTGATACGCTAAACACAT
GAAAGAGATTTACGGAGATCGCCAAGTTGTTTATGACGGAATTGACgA
AACTCTATGAAGAGTATCAAAGAGGAACCATTaGTCAACTTTTAGAGCAT
ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGtTGATGGTAA
GAGAGATaCCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTAT
TAGTAA

SEQ ID NO. 7411

STRAIN JM9130013

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACACATTACGGGA
CACTCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATGACTTTT
CGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTGTGTCAGAGGATAC
ACGAAATACGGGACTTTTACTCAAGCAGCTTTGATATTACTACTAAACAA
TTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTTAATTGAT
TTGTTAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCC
CTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGG
ATATCCCGGTGCTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTC
ATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACC
GCGTAAGCAAGGTCAACAAATAAaCTTTTGTGAAACAAGAAAGATTACC
CTGAAACACAATCTTTTATGAGTACCGGTTTCGAGTCTCTGATACGCTA
AAACACATGAAAGAGATTTATGGAGATCGCCAAGTTGTTTATGACGCGA
ATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCACTTT
TAGGGCATATTGaaaAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTT
GATGGTAAGAGAGATACTAGCGAGTGAAAGACAGTAGCCAACAAGATCC
AGTAGTATTAGTAA

PRETTY of: /biotmp/msa323014.2{*} March 28, 2003 02:40 ..

	1		50
msa323014.2{343_18RS21}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_A909}	-----	-AGTTCAAAA	AAGTTTTAAA
msa323014.2{343_COH1}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_M732}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_M781}	---aaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_2603}	atggaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_1169NT}	-----	atggaaatgc	aAGTTCAAAA
msa323014.2{343_090}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_CJB110}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_H36B}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_JM9130013}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
Consensus	*****	*****	*****

	51		100
msa323014.2{343_18RS21}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_A909}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_COH1}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_M732}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_M781}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_2603}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_1169NT}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_090}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_CJB110}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_H36B}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_JM9130013}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
Consensus	*****	*****	*****

	101		150
msa323014.2{343_18RS21}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_A909}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_COH1}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_M732}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_M781}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_2603}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_1169NT}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_090}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_CJB110}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTGTGTC	AGAGGATACA
msa323014.2{343_H36B}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTGTGTC	AGAGGATACA
msa323014.2{343_JM9130013}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTGTGTC	AGAGGATACA
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_A909}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_COH1}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_M732}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_M781}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_2603}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_1169NT}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_090}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_CJB110}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_H36B}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_JM9130013}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_A909}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_COH1}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_M732}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_M781}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_2603}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_1169NT}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_090}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_CJB110}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_H36B}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_JM9130013}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
Consensus	*****	*****	****-*****	*****	*****
msa323014.2{343_18RS21}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_A909}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_COH1}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_M732}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_M781}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_2603}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_1169NT}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_090}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_CJB110}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_H36B}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_JM9130013}	TGTTAAAAGA	AGGGGaaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
Consensus	*****	*****-*****	*****	*****	*****
msa323014.2{343_18RS21}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_A909}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_COH1}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_M732}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_M781}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_2603}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_1169NT}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_090}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_CJB110}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_H36B}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_JM9130013}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
Consensus	*****	*****	*****	*****	*****-*****
msa323014.2{343_18RS21}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_A909}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_COH1}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_M732}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_M781}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_2603}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_1169NT}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_090}	gATCCCGtTc	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_CJB110}	gATCCCGtTc	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_H36B}	tATCCCGtTc	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_JM9130013}	tATCCCGtTc	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
Consensus	-*****-***	*****	*****	*****	*****
msa323014.2{343_18RS21}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_A909}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_COH1}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_M732}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_M781}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_2603}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_1169NT}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_090}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg	
msa323014.2{343_CJB110}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg	
msa323014.2{343_H36B}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg	
msa323014.2{343_JM9130013}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg	
Consensus	*****	*****	*****	*****	*****	
msa323014.2{343_18RS21}	451	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_A909}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_COH1}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_M732}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_M781}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_2603}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_1169NT}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_090}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_CJB110}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_H36B}	CGTAAGcAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_JM9130013}	CGTAAGcAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC	
Consensus	*****~**	*****	*****~**	*****~**	*****~**	*****~**
msa323014.2{343_18RS21}	501	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
msa323014.2{343_A909}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_COH1}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_M732}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_M781}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_2603}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_1169NT}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_090}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_CJB110}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_H36B}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_JM9130013}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
Consensus	*****	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	551	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_A909}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_COH1}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_M732}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_M781}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_2603}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_1169NT}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_090}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_CJB110}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_H36B}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_JM9130013}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
Consensus	*****	*****~**	*****	*****	*****	*****
msa323014.2{343_18RS21}	601	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
msa323014.2{343_A909}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_COH1}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_M732}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_M781}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_2603}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_1169NT}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_090}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_CJB110}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_H36B}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_JM9130013}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
Consensus	*****	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	651	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_A909}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_COH1}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_M732}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_M781}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_2603}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_1169NT}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_090}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_CJB110}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_H36B}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_JM9130013}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
Consensus	**~*****	*****~****	*****	*****	*****	*****
msa323014.2{343_18RS21}	701	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_A909}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA	
msa323014.2{343_COH1}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA	
msa323014.2{343_M732}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA	
msa323014.2{343_M781}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA	
msa323014.2{343_2603}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA	

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_1169NT}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_090}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_CJB110}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_H36B}	ATGGTAAGAG	AGATACtGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_JM9130013}	ATGGTAAGAG	AGATACtGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
Consensus	*****	*****_***	*****	*****	*****
751					
msa323014.2{343_18RS21}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_A909}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_COH1}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_M732}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_M781}	cTAGTATTAG	TAAA-----	-----	-----	-----
msa323014.2{343_2603}	cTAGTATTAG	TAAAagaata	tatcgctaata	ggtgataaaa	ctaatacaagc
msa323014.2{343_1169NT}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_090}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_CJB110}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_H36B}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_JM9130013}	gTAGTATTAG	TAA-----	-----	-----	-----
Consensus	-*****	*****	*****	*****	*****
801					
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	gataaaaaaa	gtagcaaaag	aatttaattct	caatagacaa	gaactctatg
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
851					
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	ctagtttcca	tgattta	-----	-----	-----
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----
851					
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	ctagtttcca	tgattta	-----	-----	-----
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----

SEQ ID NO. 7412

STRAIN 2603 frame: 1

MEMQVQKSFKSNHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
 DITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPISIDPGHDLVKAIEGDIPV
 VSI PGASAGITALIASGLAPQPHIFYGFLPRKKGQITFFETKQDYPETQIFYESPFRVS
 DTLKHKMEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDT
 RVDSSSQDPLVLVKEIYANGDKTNQAIKKVAKEFNLNRQELYASFHDL

SEQ ID NO. 7413

STRAIN 090 frame: 1

EMQVQKSFKSNHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPISIDPGHDLVKAIEGGIPV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQITFFETKQDYPETQIFYESPFRVSD
 TLKHKMEIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDT
 VKDSSSQDPLVLV

SEQ ID NO. 7414

STRAIN A909 frame: 2

VQKSFKSNHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
 DITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPISIDPGHDLVKAIEGDIPV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQITFFETKQDYPETQIFYESPFRVSD
 TLKHKMEIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDT
 VKDSSSQDPLVLV

SEQ ID NO. 7415

STRAIN H36B frame: 1

EMQVQKSFKSNHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPISIDPGHDLVKAIEGDIPV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQITFFETKQDYPETQIFYESPFRVSD
 TLKHKMEIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDT
 VKDSSSQDPLVLV

SEQ ID NO. 7416

Table 74: Comparative Sequences relating to SAG1572

STRAIN 18RS21 frame: 1

EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7417

STRAIN M732 frame: 1

EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7418

STRAIN COH1 frame: 1

EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7419

STRAIN M781 frame: 3

MQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDI
TTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVVS
IPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDT
LKHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTERV
KDSSQQDPLVLV

SEQ ID NO. 7420

STRAIN CJB110 frame: 1

EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAIEGGI PVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7421

STRAIN 1169NT frame: 3

QVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDIT
TKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVVSI
FGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDTL
KHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTERVK
DSSQQDPLVLV

SEQ ID NO. 7422

STRAIN JM9130013 frame: 1

EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPVVLV

msa324064.2{343_18RS21}	1	-emqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	50
msa324064.2{343_A909}		----VQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_M781}		---mqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_2603}		memqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_COH1}		-emqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_M732}		-emqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_1169NT}		---qVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_090}		-emqVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_CJB110}		-emqVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_H36B}		-emqVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_JM9130013}		-emqVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
Consensus		*--*-----	**-----	*****	*****	*****	
msa324064.2{343_18RS21}	51	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGKS	LAQVSDAGMP	100
msa324064.2{343_A909}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGKS	LAQVSDAGMP	
msa324064.2{343_M781}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGKS	LAQVSDAGMP	
msa324064.2{343_2603}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGKS	LAQVSDAGMP	
msa324064.2{343_COH1}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGKS	LAQVSDAGMP	
msa324064.2{343_M732}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGKS	LAQVSDAGMP	
msa324064.2{343_1169NT}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGKS	LAQVSDAGMP	
msa324064.2{343_090}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGKS	LAQVSDAGMP	
msa324064.2{343_CJB110}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGKS	LAQVSDAGMP	
msa324064.2{343_H36B}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGKS	LAQVSDAGMP	
msa324064.2{343_JM9130013}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLLKEGKS	LAQVSDAGMP	
Consensus		*****	*****	*****	*****	*****	

Table 74: Comparative Sequences relating to SAG1572

	101				150
msa324064.2{343_18RS21}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_A909}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_M781}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_2603}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_COH1}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_M732}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_1169NT}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_090}	SISDPGHDLV	KAAIEGgIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_CJB110}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_H36B}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP
msa324064.2{343_JM9130013}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFI.P
Consensus	*****	*****_***	*****	*****	*****
	151				200
msa324064.2{343_18RS21}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_A909}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_M781}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_2603}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_COH1}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_M732}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_1169NT}	RKkGQQITFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_090}	RKkGQQITFF	ETKkDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_CJB110}	RKkGQQITFF	ETKkDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_H36B}	RKkGQQITFF	ETKkDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
msa324064.2{343_JM9130013}	RKkGQQITFF	ETKkDYPETQ	IFYESPFRVS	DTLKHMKIY	GDRQVVLVRE
Consensus	***-*****	***-*****	*****	*****	*****
	201				250
msa324064.2{343_18RS21}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_A909}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_M781}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_2603}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_COH1}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_M732}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_1169NT}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_090}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_CJB110}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_H36B}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
msa324064.2{343_JM9130013}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE	RVKDSSQQDP
Consensus	*****	*****_**	*****	*****	*****
	251				289
msa324064.2{343_18RS21}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_A909}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_M781}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_2603}	lVLVkeyian	gdktngaiikk	vakefnlnrq	elyasfhdI	
msa324064.2{343_COH1}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_M732}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_1169NT}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_090}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_CJB110}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_H36B}	lVLV-----	-----	-----	-----	-----
msa324064.2{343_JM9130013}	vVLV-----	-----	-----	-----	-----
Consensus	-*****	*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7501
STRAIN 2603
ATGAGCGTATATGTTAGTGGAAATAGGAATTATT
TCTTCTTTGGGAAAGAATTATAGCGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGA
ATTTCTAAACATTTATATAAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATA
ACTAGTGACCCAGAGGTTCTCTGAGCAATACAAAGATGAGACACGTAATTTAAATTTGCT
TTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAAAGCTTATCATAT
ATTGCTGTGTGTTTAGGACCTCACTTGGGGGAAAGAGTGCTGGTCAAATGCCTTGAT
CAATTTGAAGAAGGAGAGCGTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTAC
CATATTGCTGATGAATTTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTC
ACCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGATGGC
GATTGTGATTTAGCTATTTTGGTGGCTGTGATGAGTTAAGTGATATTTCTTTAGCAGGC
TTCACATCACTAGGAGCTATTAATACAGAAATGGCATGTGAGCCCTATTCTTCTGGAAAA
GGAATCAATTTGGGTGAGGGCGCTGTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCT
AAATATGAAAAATATTCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCT
AAGCCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGTATT
GACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGGTACTCAAGCTAATGATAAA
ATGAAAAAAATATGATGTAAGTTTTCGCCACAACGACATTGATCAGCAGTACCAAG
GGGCAACGGGTCATAGCTCTAGGGGCTGACAGGTATTATCGAATTGATTAAATGTTTAGCG
GCAATAGAGGAACAGACTGTACCACTAAATGAGATTGGGATAGAAGGTTTTCCA
GAAAAATTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTTTTCG
TTTGTCTTTGGTGGAATAATAGTGGTGTCTTATTGTCATCTTTAGATTCACTCTAGAA
ACATTACCTGCTAGAGAAATCTTAAATGGCTATCTTATCATCTGTGCTTCCATTCT
AAGAATGAATCAGTTCTTATTAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAA
GCATTACGCTTTAAAGGGGCTAGACCACCAAACTGTCAACCCAGCACAAATTTAGGAAA
ATGATGATTTTTCCAAAATGGTGGCGTAACACAGCTCAAGCACTAATAGAAAGCAAT
ATTAATCTAAAAAAACAGATACTTCAAAGTAGGAATTTGATTTACAACACTTTCTGGA
CCAGTTGAGGTTGTTGAAGGTATTGAAAAAGCAATCAACAAGAGGATATGCACATGTT
TCTGCTTCCAGATTCCGTTTACAGTAATGAAATGCAGCAGCTGGTATGCTTTCTATCATT
TTTAAAAATAACAGGTCCTTTATCTGTCATTTTCGACAAATAGTGGAGCGCTTGATGGTATA
CAATATGCCAAGGAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTCTCTGCT
AATCAGTGGACAGACAGATTGTTTATGTTGGTGGCAACAATTAACATATGATAGTCAAATG
TTTGTGCGTTCTGATTATTGTTTACGACCAAGTCCTCTCTCGTCAAGCATTGGGATAATTCT
CCTATAATATTAGGTAGTAAACAATTAATAATAGCCATAAAACATTACAGATGTGATG
ACTATTTTGTGCTGCTGCGCTCAAATTTATTTATCAGACTTAGGACTAACCATAAAAGAT
ATCAAAGGTTTCCGTTTGAATGAGCGGAAGAGGAGGAGTTAGTTTCAAGATTATGATTTCTTA
GCGAATTTGCTGATGATTATAATATGCCAAACCTTGCTTCTGGTCAGTTTGGATTTTCA
TCTAATGCTGCTGGTGAAGAAGTGGACTATAGTTAATGAAAGTATAGAAAAGGCTAT
TATTAGTCTATCTTATTCGATCTTCGGTGGTATCTCTTTGCTATTATTGAAAAAGG

SEQ ID NO. 7502
STRAIN 090
ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGaATTAT
AGCGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACA
TTTATATAAAATCAAGACTCTATTTTAGAATCTTATACAGGAAGCATAA
CTAGTGACCCAGAGGTTCTCTGAGCAATACAAAGATGAGACACGTAATTTT
AAATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAA
TTTAAAAAGCTTATCATAATATGCTGTGTGTTTAGGGACCTCACTTGGGG
GAAAGAGTGCTGGTCAAATGCCITGTATCAATTTGAAGAAGGAGAGCGT
CAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGA
TGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAA
CCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTT
CAAGATGGCGAATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAG
TGATATTTCTTTAGCAGGCTTCACTACATAGGAGCTATTATACAGAAA
TGGCATGTGAGCCCTATTCTTCTGAAAAAGGAATCAATTTGGGTGAGGGC
GCTGGTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAATATGGA
AATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTA
AGCCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAA
GCAGGTATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGG
TACTCAAGCTAATGATAAAATGGAAGAAAAATATGATGGTAAGTTTTC
CGACAACGCAATTGATCAGCAGTACCAAGGGGCAACGGGTCACTACTA
GGGGCTGCAGGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGA
ACAGACTGTACCAAGCACTAAATGAGATTGGGATAGAAGGTTTTCCAG
AAAAATTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTA
AATTTTCTGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATTGTCTATC
TTTAGATTCACTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATG
CTATCTTATCATCTGTTGCTTCCATTCTAAGAAATGAATCACTTTCTATA
ACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTT
TAAAGGGGCTAGACCACCAAACTGTCAACCCAGCACAATTTAGGAAAA
TGGATGATTTTCCAAAATGGTTGCCGTAACACAGCTCAAGCACTAATA
GAAAGCAATATTAACTAAAAAAACAAGTACTTCAAAGTAGGAATGTT
ATTTACAACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAGC
AAATCACAACAGAGGATATGCACATGTTTCTGCTTACGATTTCCGTTT
ACAGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAATAAC
AGGTCCTTTATCTGCTATTTGACAAATAGTGGAGCGCTTGATGGTATAC
AATATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTT
GTTTCTGCTAATCAGTGGACAGACATGAGTTTATGTTGGTGGCAACAAAT
AACTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAACAG
TCCTCTCTCGTCAAGCAATTGGATAATTCTCTATAATATTAGGTAGTAAA
CAATTAATAATAGCCATAAAACATTACAGATGTGATGACTATTTTGA
TGCTGCGCTTCAAATTTATTTATCAGACTTAGGACTAACCATAAAAGATA
TCAAAGGTTTCTGTTTGAATGAGCGGAAGAGGAGTTAGTTCAAGATTAT
GATTTCTTAGCGAATCTGTGAGTATTATAATATGCCAAACCTTGCTTC

Table 75: Comparative Sequences relating to SAG0671

TGGTCAGTTTGGATTTTCATCTAATGGTGTGGTGAAGAAGTGGACTATA
CTGTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTATCTTATTCG
ATCTTTGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7503

STRAIN A909

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATT
ATAGCGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAA
CAITTTATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCAT
AACTAGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATT
TTAAATTTGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTT
AATTTAAAAGCTTATCATAAATTGCTGTGTGTTTAGGGACCTCACTTGG
GGGAAAGAGTGTGGTCAAAATGCCCTGTATCAATTTGAAGAAGGAGAGC
GTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCT
GATGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTT
AACCCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTAC
TTCAGATAGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTA
AGTGATATTTCTTTAGCAGGCTTCAACATCACTAGGAGCTATTAATACAGA
AATGGCATGTGAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGG
GCGCTGGTTTGTGTCTTGTCAAAGATCAGTCTTTAGCTAAATATGGA
AAAATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACC
TAAGCCAACAGGTGAAGGGGCGGCACAGATTGCAAGCAGCTAGTGACTC
AAGCAGGTATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACA
GGTACTCAAGCTAATGATAAATGGAATAAATATGTATGGTAAGTTT
CCCGACAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCACTACTC
TAGGGGCTGACAGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAG
GAACAGACTGTACACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTCC
AGAAAATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTT
TAAATTTTTCGTTTGTCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCA
TCTTTAGATTCACTCTAGAAAACATTACCTGCTAGAGAAAAATCTTAAAT
GGCTATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTA
TAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGC
TTTAAAGGGGCTAGACCACCCAAACTGTCAACCCAGCACATTTAGGAA
AATGGATGATTTTCCAAAATGGTTGCCGTAAACAGCTCAAGCACTAA
TAGAAAGCAATAATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAATT
GTATTTACAAACATTTCTGACCAGTTGAGGTTGTGAAGGTATTGAAAA
GCAAAATCAACACAGAAGGATATGCATGTTTCTGCTTCAAGATTCCCGT
TTACAGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAAATA
ACAGGTCCTTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGATGGTAT
ACAAATATGCCAAGGAAATGATGCGTAAACGATAATCTAGACTATGTGATTC
TTGTTTCTGCTAATCAGTGGACAGACATGAGTTTATGTGTGGGCAACA
TTAACTATGATAGTCAAAATGTTTGTCCGTTCTGATTATTGTTCAACACA
AGTCTCTCTCTCGTCAAGCATTGGATAAATCTCTATAATATTAGGTAGTA
AACAAATAAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTT
GATGCTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGA
TATCAAGGTTTTCGTTTGAAGTGAAGCGGAAGGACAGTTAGTTCAAGATT
ATGATTTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCT
TCTGGTCAAGTTTGGATTTCATCTAATGGTGTGGTGAAGAAGTGGACTA
TACTGTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTTATT
CGATCTTCGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7504

STRAIN H36B

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGA
GCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTAT
ATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACTAGT
GACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAAATT
TGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAA
AAGCTTATCATAAATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAG
AGTGTGGTCAAAATGCCCTGTATCAATTTGAAGAAGGAGAGCGTCAAGT
AGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGAAT
TGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCC
TGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGA
TGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTGATA
TTCTTTAGCAGGCTTCAACATCACTAGGAGCTATTAATACAGAAATGGCA
TGTCAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGGGCGCTGG
TTTTGTGTCTTGTCAAAGATCAGTCTTAGCTAAATATGGAATAATTA
TCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGCCA
ACAGGTGAAGGGGCGGCACAGATTGCAAGCAGCTAGTGACTCAAGCAGG
TATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGGTACTC
AAGCTAATGATAAATGGAATAAATATGTATGGTAAGTTTTCCTGACA
ACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCACTCTAGGGGC
TGCAGGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGAACAGA
CTGTACCAAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAAAAT
TTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTT
TTCGTTTGTCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCTATCTTAG
ATTACCTCTAGAAAACATTACCTGCTAGAGAAAAATCTTAAATGGCTATC
TTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTA
TGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAAAG
GGGCTAGACCACCCAAACTGTCAACCCAGCACAAATTTAGGAAAATGGAT
GATTTTTTCCAAAATGGTTGCCGTAAACAGCTCAAGCACTAATAGAAAAG
CAATATTAACTCAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATTTA
CAACACTTTCTGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAATC

Table 75: Comparative Sequences relating to SAG0671

ACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACAGT
AATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAATAACAGGTC
CTTTATCTGTCTATTTCCGACAAATAGTGGAGCGCTTGATGGTATACAAAT
GCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTTCTGTTTC
TGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAACT
ATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTCCAGCACAAGTCCTC
TCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAACAATT
AAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATGCTG
CGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCAAA
GGTTTCGTTTGAATGAGCGGAAGAGGCAGTTAGTTTCAATTTATGATTT
CTTAGCGAATCTGTCTGAGTATTATAATATGCCAACCTTGCTTCTGGTC
AGTTTGGATTTTCATCTAATGGTGTGCTGGTGAAGAACTGGACTATCTGTT
AATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATTTCTGATCTT
CGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7505

STRAIN 18RS21

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATTT
ATATAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
GTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAA
TTTGTCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCAGTTGGGGGA
AGAGTGTGCTGGTCAAAATGCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
GTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGA
ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
CCTGTTCTGCAAGTAATAATGCGTAATAATTAGGAACACAATTACTTCAA
GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAAATACAGAAATGG
CATGTCAGCCCTATTCTTCTGGAAGGAATCAATTTGGGTGAGGGCGCT
GGTTTGTGTTCTTGTCAAAGATCAGTCTCTAGCTAAATATGGAATAAT
TATCGGTGCTTATTACTTTCAGATGGTTATCATATAACAGCACCTTAAGC
CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
GGTATTGACTACAGTGAAGTTGACTATATTAAACGGTACCGGTACAGGTAC
TCAAGCTAATGATAAAATGGAATAAATATGATGGTAAGTTTTCCTCGA
CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGGG
GCTGCAGGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGAACA
GACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAA
ATTTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
TTTTGCTTTGCTTTTGGTGAATAATAGTGGTGTCTTATTGTCTATCTTT
AGATTACCTCTAGAAACATTACCTGCTAGAGAAATCTTAAATGGCTA
TCTTATCATCTGTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
AGGGGCTAGACCCCAAACTGTCAACCCAGCACAATTTAGGAAAATGG
ATGATTTTTCCAAAATGGTTGCGGTAACAACAGCTCAAGCACTAATAGAA
AGCAATATTAACTTAAAAAACAAGATACTTCAAAGTAGGAATTGTATT
TACAACACTTTCTGGACAGTTGAGGTGTTGAAGGTATTGAAAAGCAAA
TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCGTTTACA
GTAATGAATGCAAGCAGCTGGTATGCTTTCTATCATTTTAAATAACAGG
TCCTTTATCTGTCATTTGCAAAATAGTGGAGCGCTTGATGGTATACAAT
ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
TCTGTCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTA
CTATGATGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAGCACAAGTCC
TCTCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAACAA
TTAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATGC
TGCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
AAGGTTTCGTTTGAATGAGCGGAAGAGGCAGTTAGTTTCAATTTATGAT
TTCTTAGCGAATCTGTCTGAGTATTATAATATGCCAACCTTGCTTCTGG
TCAGTTTGGATTTTTCATCTAATGGTGTGCTGGTGAAGAACTGGACTATCTG
TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATTTCTGATCT
TTCGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7506

STRAIN M732

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAG
CGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
TATATAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACT
AGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAA
ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
TAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCAGTTGGGGGA
AAGAGTGTGCTGGTCAAAATGCTTGTATCAATTTGAAGAAGGAGAGCGTCA
AGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATG
AATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACC
GCCTGTTCTGCAAGTAATAATGCCGTAATAATTAGGAACACAATTACTTCA
AGATGGCGATTGTGATTTAGCTATTGTTGGTGGCTGTGATGAGTTAAGTG
ATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAAATACAGAAATG
GCATGTCAGCCCTATTCTTCTGGAAGGAATCAATTTGGGTGAGGGCGC
TGGTTTGTGTTCTTGTCAAAGATCAGTCTTCTAGCTAAATATGGAATAA
TTATCGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTTAAG
CCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGC
AGGTATTGACTACAGTGAAGTTGACTATATTAAACGGTACCGGTACAGGTA
CTCAAGCTAATGATAAAATGGAATAAATATGATGGTAAGTTTTCCTCGG
ACAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGG

Table 75: Comparative Sequences relating to SAG0671

GGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAAC
 AGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTCCAGAA
 AATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAA
 TTTTTCGTTTGGCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCT
 TAGATTACCTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAAC
 CTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTA
 AAGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAATTTAGGAAAATG
 GATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
 AAGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTAT
 TTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 ATCACAACAGAAGGATATGCACATGTTTCTGCTTCAAGATTCCCGTTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTTAAATAACAG
 GTCCTTTATCTGTCATTTTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 TATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 ACTATGATAGTCAAAATGTTTGTGCGTTCTGATTATTGTTCAAGCAAGTC
 CTCTCTCGTCAAGCATTGGATAAATCTCCTATAATATTAGGTAGTAAACA
 ATTAAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTGTATG
 CTGCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATC
 AAAGGTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTCAAGATTATGA
 TTTCTAGCGAAGCTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTG
 GTCAGTTTGGATTTCATCTAATGGTGTGCTGGAAGAACTGGACTataCT
 GTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTTATTCGAT
 CTTCCGGTGGTATCTCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7507

STRAIN COH1

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
 ATATAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCACCCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATGG
 CATGTCAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGAAAAAAT
 TATCGGTGGTCTTATTAATTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTACCGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGAAAAAATATGTATGGTAAGTTTTCCTCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACCGGTCATCTCTAGGG
 GCTGCAAGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGAACA
 GACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTT
 AGATTACCTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAATTTAGGAAAATGG
 ATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTATT
 TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCAAGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTTAAATAACAGG
 TCCTTTATCTGTCATTTTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAAATGTTTGTGCGTTCTGATTATTGTTCAAGCAAGTCC
 TCTCTCGTCAAGCATTGGATAAATCTCCTATAATATTAGGTAGTAAACAA
 TTAATAATAGCCATAAAACATTCACAGATGTGATGACTATTTTGTATGC
 TGGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
 AAGGTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTCAAGATTATGAT
 TTTCTAGCGAAGCTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTGCTGGAAGAACTGGACTATCTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTTATTCGATC
 TCGGTGGTATCTCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7508

STRAIN M781

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
 ATATAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA

Table 75: Comparative Sequences relating to SAG0671

ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGG
 CATGTGAGCCCTATTCTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAATAAT
 TATCGGTGGTCTTATTAATTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAATAAATATGTATGGTAAGTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGAACA
 GACTGTACAGCACTAAATAAGAGATTGGGATAGAAGGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATTGTCTATCTT
 AGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTCTATAACC
 TATGAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCAACCAAACTGTCAACCCAGCACAAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACCAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTATT
 TACAACACTTTCTGGACAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTACGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAATAACAGG
 TCCCTTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAAATGTTTGTGGTCTGATTATTGTTTCAACAGTCC
 TCTCTCGTCAAGCATTGGGATAATCTCCTATAATATTAGGTAGTAAACAA
 TTAATAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATGC
 TGGCCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAGATATCA
 AAGGTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTTCAAGTTATGAT
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTGGTGAAGAACTGGACTATAGTCT
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTATTTCGATC
 TTTGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7509

STRAIN CJB110

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAAATTATAGC
 GAGCATAAAGCAGCATCTCTCGACTTAAAGAAAGGAATTTCTAAACATTT
 ATATAAATAACAGCAGCTCTATTTTGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGTCTTCTCAGGTGTTAATTT
 AAAAGCTTATCATAAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTCTGGTCAAAATGCCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTAATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTATAACAGAAATGG
 CATGTGAGCCCTATTCTCTGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAATAAT
 TATCGGTGGTCTTATTAATTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAATAAATATGTATGGTAAGTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGAACA
 GACTGTACAGCACTAAATAAGAGATTGGGATAGAAGGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATTGTCTATCTT
 AGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTCTATAACC
 TATGAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCAACCAAACTGTCAACCCAGCACAAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACCAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTATT
 TACAACACTTTCTGGACAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTACGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAATAACAGG
 TCCCTTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAAATGTTTGTGGTCTGATTATTGTTTCAACAGTCC
 TCTCTCGTCAAGCATTGGGATAATCTCCTATAATATTAGGTAGTAAACAA
 TTAATAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATGC
 TGGCCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAGATATCA
 AAGGTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTTCAAGTTATGAT
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTGGTGAAGAACTGGACTATAGTCT
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTATTTCGATC
 TTTGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7510

STRAIN 1169NT

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAG
 CGAGCATAAACAGCATCTCTTCGACTTAAAGAAAGGAATTTCTAAACATT
 TATATAAAAATCAGGACTCTATTTTAGAATCTTATACAGGAAGCATAACT
 AGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAA
 ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
 TAAAAGCTTATCATAAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGA
 AAGAGTGTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCA
 AGTAGATGCTAGTTTATAGAAAAAGCATCTGTTTACCATATTGCTGATG
 AATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACC
 GCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCA
 AGATGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTG
 ATATTTCTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATG
 GCATGTGAGCCCTATTCTTCTGGAAGAAAGGAATCAATTTGGGTGAGGGCGC
 TGGTTTGTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAGAAA
 TTATCGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTAAG
 CCAACAGGTGAAGGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGC
 AGGTATTGACTACAGTGAGATTGACTATATTACGGTCACGGTACAGGTA
 CTCAAGCTAATGATAAAATGGAAGAAATATGTTAGTTAAGTTTTCCTCG
 ACAACGACATTGATCAGCAGTACCAAGGGGCAACCGGTCATACTTAGG
 GGCTGCAGGTATTATCGAATTGATTAAATGTTTTCGCGCAATAGAGGAAC
 AGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAAGTTTTCAGAA
 AATTTTGTCTATCATCAAAGAGAGAATACCAATAAGAAATGCTTTAA
 TTTTTCGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATTGTCTATCTT
 TAGATTCACTCTAGAAACATTACCTGCTAGAGAAATCTTAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTTCTATAAC
 CTATGAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCAATTACGCTTTA
 AAGGGGCTAGACCACCCAAACTGTCAACCCAGCACAAATTTAGGAAATG
 GATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
 AAGCAATATTAATCTAAAAACAAGATACTTCAAAGTAGGAATTGTAT
 TTACAACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 ATCACAACAGAAGGATATGCACATGTTCTGCTTCACGATTCCCGTTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAATAACAG
 GTCCTTTATCTGTCAATTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 TATGCCAAGGAATGATGCGTAACAGATAATCTAGACTATGTGATTCTTGT
 TTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTA
 ACTATGATAGTCAAATGTTTGTGGTCTGATTATTGTTTCAGCACAGTC
 CTCTCTCGTCAAGCAATTGGATAATTCTCCTATAATATTAGGTAGTAAACA
 ATTTAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATG
 CTGCGCTTCAAATTTTATATCAGACTTAGGACTAACCATAAAGATATC
 AAAGGTTTTCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAGATTATGA
 TTTCTTAGCGAATCTGTCTGAGTATTATAATATGCCAACCTTGCTCTG
 GTCAGTTTGGATTTCATCTAATGGTGGCTGGTGAAGAACTGGACTATACT
 GTTAATGAAGTATAGAAAAGGGCTATTATTAGTCTTATCTTATTCGAT
 CTTTGGTGGTATCTCTTTTGGCTATTATTGAAAAAAG

SEQ ID NO. 7511

STRAIN JM9130013

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGAG
 CATAAACAGCATCTCTTCGACTTAAAGAAAGGAATTTCTAAACATTATATA
 TAAAAATCAGGACTCTATTTTAGAATCTTATACAGGAAGCATAACTAGTG
 ACCGAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAAATTT
 GCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAA
 AGCTTATCATAAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGAAAGA
 GTGCTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAAGTA
 GATGCTAGTTTATAGAAAAAGCATCTGTTTACCATATTGCTGATGAATT
 GATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCTT
 GTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGAT
 GGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTGATAT
 TTCTTTAGCAGGCTTACATCACTAGGAGCTATTAAACAGAAATGGCAT
 GTCAGCCCTATTCTCTGGAAGAAAGGAATCAATTTGGGTGAGGGCGCTGGT
 TTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAGAAATAT
 CGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTAAGCCAA
 CAGGTGAAGGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGT
 ATTGACTACAGTGAGATTGACTATATTACGGTCACGGTACAGGTACTCA
 AGCTAATGATAAAATGGAAGAAATATGTTAGTTAAGTTTTCCTCGACAA
 CGACATTGATCAGCAGTACCAAGGGGCAACCGGTCATACTCTAGGGGCT
 GCAGGTATTATCGAATTGATTAAATTTTTCGCGCAATAGAGGAACAGAC
 TGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAAAAT
 TTGTCTATCATCAAAGAGAGAATACCAATAAGAAATGCTTTAAATTTT
 TCGTTTGTCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCTCTTTAGA
 TTCACCTCTAGAAACATTACCTGCTAGAGAAATCTTAAATGGCTATCT
 TATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTAT
 GAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCAATTACGCTTTAAAGG
 GGCTAGACCACCCAAACCTGTCAACCCAGCACAAATTTAGGAAATGGATG
 ATTTTTCAAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAAAGC
 AATATTAAATCTAAAAACAAGATACTTCAAAGTAGGAATTGTATTAC
 AACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAAGCAATCA
 CAACAGAGGATATGCACATGTTCTGCTTTCAGGATTCCCGTTTACAGTA
 ATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAATAACAGGTCC
 TTTATCTGTCAATTCGACAAATAGTGGAGCGCTTGATGGTATACAAATATG

Table 75: Comparative Sequences relating to SAG0671

CCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTTCCT
 GCTAATCAGTGGACAGACATGAGTTTATGTTGGTGGCAACAATTAACCTA
 TGATAGTCAAATCTTTGTCGGTTCGATTATTGTTTACGACACAGTCCTCT
 CTCGTCAAGCATGGATAATTCTCCTATAATATTAGGTAGTAAACAATTA
 AAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTGCTGCG
 GCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAGATATCAAAG
 GTTTCTGTTTGAATGAGCGGAAGAGGCAGTTAGTTTCAAGATTATGATTTC
 TTAGCGAAGCTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGGTCA
 GTTTGGATTTCATCTAATGGTGTCTGGTGAAGAACTGGACTATACGTGA
 ATGAAAGTATAGAAAGGGCTATTATTAGTCCTATCTTATTGATCTTC
 GGTGTATCTCTTTGCTATTATTGAAAAAAGG

PRETTY of: /biotmp/msa118688.2{*} April 9, 2003 02:55 ..

	1				50
msa118688.2{361_18RS21}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_A909}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_COH1}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_H36B}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_JM9130013}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_M732}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{GBS361_2603}	atgagcgtat	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_090}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_1169NT}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_CJB110}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_M781}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
Consensus	*****	*****	*****	*****	*****
	51				100
msa118688.2{361_18RS21}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_A909}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_COH1}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_H36B}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_JM9130013}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_M732}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{GBS361_2603}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_090}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_1169NT}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_CJB110}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_M781}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
Consensus	*****	*****	*****	*****	*****
	101				150
msa118688.2{361_18RS21}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_A909}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_COH1}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_H36B}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_JM9130013}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_M732}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{GBS361_2603}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_090}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_1169NT}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_CJB110}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_M781}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
Consensus	*****	*****	*****	*****	*****
	151				200
msa118688.2{361_18RS21}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_A909}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_COH1}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_H36B}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_JM9130013}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_M732}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{GBS361_2603}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_090}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_1169NT}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_CJB110}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_M781}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa118688.2{361_18RS21}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_A909}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_COH1}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_H36B}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_JM9130013}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_M732}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{GBS361_2603}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_090}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_1169NT}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_CJB110}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_M781}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
Consensus	*****	*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

	251		300
msa118688.2{361_18RS21}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_A909}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_COH1}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_H36B}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_JM9130013}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_M732}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{GBS361_2603}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_090}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_1169NT}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_CJB110}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_M781}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_A909}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_COH1}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_H36B}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_JM9130013}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_M732}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{GBS361_2603}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_090}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_1169NT}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_CJB110}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_M781}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_A909}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_COH1}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_H36B}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_JM9130013}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_M732}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{GBS361_2603}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_090}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_1169NT}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_CJB110}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_M781}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_A909}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_COH1}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_H36B}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_JM9130013}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_M732}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{GBS361_2603}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_090}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_1169NT}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_CJB110}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_M781}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_A909}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_COH1}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_H36B}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_JM9130013}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_M732}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{GBS361_2603}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_090}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_1169NT}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_CJB110}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_M781}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_A909}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_COH1}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_H36B}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_JM9130013}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_M732}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{GBS361_2603}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_090}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_1169NT}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_CJB110}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_M781}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
Consensus	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

Consensus	*****	*****	*****	*****	*****
	551				600
msa118688.2{361_18RS21}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_A909}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_COH1}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_H36B}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_JM9130013}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_M732}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{GBS361_2603}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_090}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_1169NT}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_CJB110}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_M781}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
Consensus	*****	*****	*****	*****	*****
	601				650
msa118688.2{361_18RS21}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_A909}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_COH1}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_H36B}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_JM9130013}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_M732}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{GBS361_2603}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_090}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_1169NT}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_CJB110}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_M781}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
Consensus	*****	*****	*****	*****	*****
	651				700
msa118688.2{361_18RS21}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_A909}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_COH1}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_H36B}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_JM9130013}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_M732}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{GBS361_2603}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_090}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_1169NT}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_CJB110}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_M781}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
Consensus	*****	*****	*****	*****	*****
	701				750
msa118688.2{361_18RS21}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_A909}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_COH1}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_H36B}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_JM9130013}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_M732}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{GBS361_2603}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_090}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_1169NT}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_CJB110}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_M781}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
Consensus	*****	*****	*****	*****	*****
	751				800
msa118688.2{361_18RS21}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_A909}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_COH1}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_H36B}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_JM9130013}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_M732}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{GBS361_2603}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_090}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_1169NT}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_CJB110}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_M781}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
Consensus	*****	*****	*****	*****	*****
	801				850
msa118688.2{361_18RS21}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_A909}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_COH1}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_H36B}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_JM9130013}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_M732}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{GBS361_2603}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_090}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_1169NT}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_CJB110}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_M781}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAT	GGTCACGGTA
Consensus	*****	*****	*****	*****	*****
	851				900
msa118688.2{361_18RS21}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_A909}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_COH1}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_H36B}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_JM9130013}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_M732}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{GBS361_2603}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_090}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_1169NT}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_CJB110}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_M781}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
Consensus	*****	*****	*****	*****	*****
	901				950
msa118688.2{361_18RS21}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_A909}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_COH1}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_H36B}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_JM9130013}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_M732}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{GBS361_2603}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_090}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_1169NT}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_CJB110}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_M781}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
Consensus	*****	*****	*****	*****	*****
	951				1000
msa118688.2{361_18RS21}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_A909}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_COH1}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_H36B}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_JM9130013}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_M732}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{GBS361_2603}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_090}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_1169NT}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_CJB110}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_M781}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa118688.2{361_18RS21}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_A909}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_COH1}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_H36B}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_JM9130013}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_M732}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{GBS361_2603}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_090}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_1169NT}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_CJB110}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_M781}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa118688.2{361_18RS21}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_A909}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_COH1}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_H36B}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_JM9130013}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_M732}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{GBS361_2603}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_090}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_1169NT}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_CJB110}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_M781}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa118688.2{361_18RS21}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_A909}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_COH1}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_H36B}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_JM9130013}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_M732}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{GBS361_2603}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_090}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_1169NT}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_M781}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
Consensus	*****	*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_CJB110}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	aTCTTATTGT		
msa118688.2{361_M781}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	aTCTTATTGT		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1151	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	1200
msa118688.2{361_A909}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_COH1}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_H36B}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_JM9130013}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_M732}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{GBS361_2603}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_090}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_1169NT}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_CJB110}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_M781}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1201	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	1250
msa118688.2{361_A909}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_COH1}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_H36B}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_JM9130013}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_M732}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{GBS361_2603}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_090}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_1169NT}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_CJB110}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_M781}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1251	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC	1300
msa118688.2{361_A909}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_COH1}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_H36B}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_JM9130013}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_M732}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{GBS361_2603}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_090}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_1169NT}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_CJB110}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_M781}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1301	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG	1350
msa118688.2{361_A909}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_COH1}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_H36B}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_JM9130013}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_M732}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{GBS361_2603}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_090}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_1169NT}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_CJB110}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_M781}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1351	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT	1400
msa118688.2{361_A909}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_COH1}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_H36B}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_JM9130013}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_M732}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{GBS361_2603}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_090}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_1169NT}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_CJB110}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_M781}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1401	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA	1450
msa118688.2{361_A909}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_COH1}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_H36B}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_JM9130013}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_M732}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{GBS361_2603}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_090}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_1169NT}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_CJB110}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_M781}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1451	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA	1500
msa118688.2{361_A909}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_COH1}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_H36B}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_JM9130013}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_M732}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{GBS361_2603}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_090}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_1169NT}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_CJB110}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
msa118688.2{361_M781}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1501	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC	1550
msa118688.2{361_A909}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_COH1}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_H36B}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_JM9130013}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_M732}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{GBS361_2603}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_090}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_1169NT}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_CJB110}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
msa118688.2{361_M781}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1551	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA	1600
msa118688.2{361_A909}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_COH1}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_H36B}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_JM9130013}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_M732}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{GBS361_2603}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_090}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_1169NT}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_CJB110}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
msa118688.2{361_M781}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1601	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT	1650
msa118688.2{361_A909}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_COH1}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_H36B}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_JM9130013}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_M732}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{GBS361_2603}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_090}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_1169NT}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_CJB110}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
msa118688.2{361_M781}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1651	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT	1700
msa118688.2{361_A909}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_COH1}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_H36B}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_JM9130013}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_M732}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{GBS361_2603}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_090}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_1169NT}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_CJB110}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
msa118688.2{361_M781}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1701	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC	1750
msa118688.2{361_A909}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC		
msa118688.2{361_COH1}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC		
msa118688.2{361_H36B}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC		
msa118688.2{361_JM9130013}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC		
msa118688.2{361_M732}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC		
msa118688.2{GBS361_2603}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC		

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_090}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC		
msa118688.2{361_1169NT}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC		
msa118688.2{361_CJB110}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC		
msa118688.2{361_M781}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1751	AATTAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	1800	TTGTTTCAGCA
msa118688.2{361_A909}	AATTAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA		
msa118688.2{361_COH1}	AATTAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA		
msa118688.2{361_H36B}	AATTAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA		
msa118688.2{361_JM9130013}	AATTAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA		
msa118688.2{361_M732}	AATTAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA		
msa118688.2{GBS361_2603}	AATTAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA		
msa118688.2{361_090}	AATTAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA		
msa118688.2{361_1169NT}	AATTAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA		
msa118688.2{361_CJB110}	AATTAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA		
msa118688.2{361_M781}	AATTAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1801	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	1850	TATTAGGTAG
msa118688.2{361_A909}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG		
msa118688.2{361_COH1}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG		
msa118688.2{361_H36B}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG		
msa118688.2{361_JM9130013}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG		
msa118688.2{361_M732}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG		
msa118688.2{GBS361_2603}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG		
msa118688.2{361_090}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG		
msa118688.2{361_1169NT}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG		
msa118688.2{361_CJB110}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG		
msa118688.2{361_M781}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1851	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	1900	ATGACTATTT
msa118688.2{361_A909}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT		
msa118688.2{361_COH1}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT		
msa118688.2{361_H36B}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT		
msa118688.2{361_JM9130013}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT		
msa118688.2{361_M732}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT		
msa118688.2{GBS361_2603}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT		
msa118688.2{361_090}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT		
msa118688.2{361_1169NT}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT		
msa118688.2{361_CJB110}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT		
msa118688.2{361_M781}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1901	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	1950	AACCATAAAA
msa118688.2{361_A909}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA		
msa118688.2{361_COH1}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA		
msa118688.2{361_H36B}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA		
msa118688.2{361_JM9130013}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA		
msa118688.2{361_M732}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA		
msa118688.2{GBS361_2603}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA		
msa118688.2{361_090}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA		
msa118688.2{361_1169NT}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA		
msa118688.2{361_CJB110}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA		
msa118688.2{361_M781}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1951	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	2000	TTAGTTTCAGA
msa118688.2{361_A909}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA		
msa118688.2{361_COH1}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA		
msa118688.2{361_H36B}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA		
msa118688.2{361_JM9130013}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA		
msa118688.2{361_M732}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA		
msa118688.2{GBS361_2603}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA		
msa118688.2{361_090}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA		
msa118688.2{361_1169NT}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA		
msa118688.2{361_CJB110}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA		
msa118688.2{361_M781}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTTCAGA		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	2001	TTATGATTTT	TTAGCGAAGT	TGTCTGAGTA	TTATAATATG	2050	CCAAACCTTG
msa118688.2{361_A909}	TTATGATTTT	TTAGCGAAGT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG		
msa118688.2{361_COH1}	TTATGATTTT	TTAGCGAAGT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG		
msa118688.2{361_H36B}	TTATGATTTT	TTAGCGAAGT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG		
msa118688.2{361_JM9130013}	TTATGATTTT	TTAGCGAAGT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG		
msa118688.2{361_M732}	TTATGATTTT	TTAGCGAAGT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG		

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{GBS361_2603}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_090}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_1169NT}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_CJB110}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_M781}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
Consensus	*****	*****	*****	*****	*****
2051					
msa118688.2{361_18RS21}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_A909}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_COH1}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_H36B}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_JM9130013}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_M732}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{GBS361_2603}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_090}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_1169NT}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_CJB110}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_M781}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
Consensus	*****	*****	*****	*****	*****
2101					
msa118688.2{361_18RS21}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_A909}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_COH1}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_H36B}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_JM9130013}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_M732}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{GBS361_2603}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_090}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_1169NT}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_CJB110}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_M781}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
Consensus	*****	*****	*****	*****	*****
2151					
msa118688.2{361_18RS21}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_A909}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_COH1}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_H36B}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_JM9130013}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_M732}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{GBS361_2603}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_090}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_1169NT}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_CJB110}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_M781}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
Consensus	*****	*****	*****	*****	***

SEQ ID NO. 7512

STRAIN 2603 frame: 1

MSVYVSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQ
 YKDETRNFKAFAFEALASSGVNLKAYHNIACVCLGTSLGKKSAGQNALYQFEEGERQV
 DASLLEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDQDCLDAICGG
 CDELSDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYKGIIGGL
 ITSDGYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKF
 FPTTLISSTKGQTGHTLGAAGIIELINCLAAIEEQVTPATKNEIGIEGFENFVYHQKR
 EYPRNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITY
 EKVASNFDFEALRFKGRPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTS
 KVGIVFTTSLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSV
 ISTNSGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWQQNLNYSQMFVGS DYCSA
 QVLSRQALDNP IILGSKQLKYSKHTFTDVTI FDAALQNLSDGLTI IKDIKGFVWNER
 KKA VSSDYDFLANLSEYNNMPLNASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIF
 GGISFAIIEKR

SEQ ID NO. 7513

STRAIN 090 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
 TRNFKAFAFEALASSGVNLKAYHNIACVCLGTSLGKKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDQDCLDAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFPTT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQVTPATKNEIGIEGFENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEYKVA
 SNFDFEALRFKGRPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGIV
 VFTTSLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWQQNLNYSQMFVGS DYCSAQVLS
 RQALDNP IILGSKQLKYSKHTFTDVTI FDAALQNLSDGLTI IKDIKGFVWNERKKA
 VSSDYDFLANLSEYNNMPLNASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIFGGIS
 FAIIEKR

SEQ ID NO. 7514

STRAIN A909 frame: 3

Table 75: Comparative Sequences relating to SAG0671

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTSLGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHI ADEL MAYHDI VGASYVISTAC SASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKI IGG LITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFK GARPPKTVNPAQFRKMDDFSKMVA VTTAQA LIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNL LSDLGLTI KD IKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYISFGGIS
 FAIIEKR

SEQ ID NO. 7515

STRAIN H36B frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTSLGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHI ADEL MAYHDI VGASYVISTAC SASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKI IGG LITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFK GARPPKTVNPAQFRKMDDFSKMVA VTTAQA LIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNL LSDLGLTI KD IKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYISFGGIS
 FAIIEKR

SEQ ID NO. 7516

STRAIN 18RS21 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTSLGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHI ADEL MAYHDI VGASYVISTAC SASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKI IGG LITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFK GARPPKTVNPAQFRKMDDFSKMVA VTTAQA LIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNL LSDLGLTI KD IKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYISFGGIS
 FAIIEKR

SEQ ID NO. 7517

STRAIN M732 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTSLGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHI ADEL MAYHDI VGASYVISTAC SASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKI IGG LITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFK GARPPKTVNPAQFRKMDDFSKMVA VTTAQA LIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNL LSDLGLTI KD IKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYISFGGIS
 FAIIEKR

SEQ ID NO. 7518

STRAIN COH1 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTSLGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHI ADEL MAYHDI VGASYVISTAC SASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKI IGG LITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFK GARPPKTVNPAQFRKMDDFSKMVA VTTAQA LIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNL LSDLGLTI KD IKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYISFGGIS
 FAIIEKR

SEQ ID NO. 7519

STRAIN M781 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTSLGGKSAGQNALYQFEEGERQVDASL

Table 75: Comparative Sequences relating to SAG0671

LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPFIILGSKQLKYSHKFTDVTMTIFDAALQNLSDGLGTIKDIGFVWNERKKAV
SSDYDFLANLSEYNNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7520

STRAIN CJB110 frame: 3

VSGIGIISLGGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPFIILGSKQLKYSHKFTDVTMTIFDAALQNLSDGLGTIKDIGFVWNERKKAV
SSDYDFLANLSEYNNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7521

STRAIN 1169NT frame: 3

VSGIGIISLGGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPFIILGSKQLKYSHKFTDVTMTIFDAALQNLSDGLGTIKDIGFVWNERKKAV
SSDYDFLANLSEYNNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7522

STRAIN JM9130013 frame: 3

VSGIGIISLGGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPFIILGSKQLKYSHKFTDVTMTIFDAALQNLSDGLGTIKDIGFVWNERKKAV
SSDYDFLANLSEYNNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIEKR

PRETTY of: /biotmp/msa118713.2{*} April 9, 2003 02:54 ..

	1	50
msa118713.2{361_090}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS	
msa118713.2{361_1169NT}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS	
msa118713.2{361_CJB110}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS	
msa118713.2{361_M781}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS	
msa118713.2{361_18RS21}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS	
msa118713.2{361_A909}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS	
msa118713.2{361_COH1}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS	
msa118713.2{361_H36B}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS	
msa118713.2{361_JM9130013}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS	
msa118713.2{361_M732}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS	
msa118713.2{GBS361_2603}	msvYVSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS	
Consensus	*****	*****
	51	100
msa118713.2{361_090}	ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL	
msa118713.2{361_1169NT}	ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL	
msa118713.2{361_CJB110}	ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL	
msa118713.2{361_M781}	ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL	
msa118713.2{361_18RS21}	ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL	

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_A909}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_COH1}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_H36B}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_JM9130013}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_M732}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{GBS361_2603}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_1169NT}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_CJB110}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_M781}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_18RS21}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_A909}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_COH1}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_H36B}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_JM9130013}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_M732}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{GBS361_2603}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_1169NT}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_CJB110}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_M781}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_18RS21}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_A909}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_COH1}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_H36B}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_JM9130013}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_M732}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{GBS361_2603}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_1169NT}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_CJB110}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_M781}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_18RS21}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_A909}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_COH1}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_H36B}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_JM9130013}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_M732}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{GBS361_2603}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_1169NT}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_CJB110}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_M781}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_18RS21}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_A909}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_COH1}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_H36B}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_JM9130013}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_M732}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{GBS361_2603}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_1169NT}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_CJB110}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_M781}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_18RS21}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_A909}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_COH1}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_H36B}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_JM9130013}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_M732}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{GBS361_2603}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	PENFVYHQKR	EYPIRNALNF	SFAPGGNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_1169NT}	PENFVYHQKR	EYPIRNALNF	SFAPGGNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_CJB110}	PENFVYHQKR	EYPIRNALNF	SFAPGGNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_M781}	PENFVYHQKR	EYPIRNALNF	SFAPGGNSG	ILLSSLDSP	ETLPARENLK

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_18RS21}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
msa118713.2{361_A909}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
msa118713.2{361_COH1}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
msa118713.2{361_H36B}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
msa118713.2{361_JM9130013}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
msa118713.2{361_M732}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
msa118713.2{GBS361_2603}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK		
Consensus	*****	*****	*****	*****	*****		
msa118713.2{361_090}	401	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR	450
msa118713.2{361_1169NT}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_CJB110}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_M781}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_18RS21}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_A909}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_COH1}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_H36B}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_JM9130013}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{361_M732}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
msa118713.2{GBS361_2603}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVNPAQFR		
Consensus	*****	*****	*****	*****	*****		
msa118713.2{361_090}	451	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE	500
msa118713.2{361_1169NT}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_CJB110}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_M781}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_18RS21}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_A909}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_COH1}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_H36B}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_JM9130013}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{361_M732}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
msa118713.2{GBS361_2603}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTSL	GPVEVVEGIE		
Consensus	*****	*****	*****	*****	*****		
msa118713.2{361_090}	501	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG	550
msa118713.2{361_1169NT}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_CJB110}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_M781}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_18RS21}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_A909}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_COH1}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_H36B}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_JM9130013}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{361_M732}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
msa118713.2{GBS361_2603}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG		
Consensus	*****	*****	*****	*****	*****		
msa118713.2{361_090}	551	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA	600
msa118713.2{361_1169NT}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA		
msa118713.2{361_CJB110}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA		
msa118713.2{361_M781}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA		
msa118713.2{361_18RS21}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA		
msa118713.2{361_A909}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA		
msa118713.2{361_COH1}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA		
msa118713.2{361_H36B}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA		
msa118713.2{361_JM9130013}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA		
msa118713.2{361_M732}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA		
msa118713.2{GBS361_2603}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA		
Consensus	*****	*****	*****	*****	*****		
msa118713.2{361_090}	601	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTITK	650
msa118713.2{361_1169NT}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTITK		
msa118713.2{361_CJB110}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTITK		
msa118713.2{361_M781}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTITK		
msa118713.2{361_18RS21}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTITK		
msa118713.2{361_A909}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTITK		
msa118713.2{361_COH1}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTITK		
msa118713.2{361_H36B}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTITK		
msa118713.2{361_JM9130013}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTITK		
msa118713.2{361_M732}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTITK		
msa118713.2{GBS361_2603}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTITK		
Consensus	*****	*****	*****	*****	*****		
msa118713.2{361_090}	651	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD	700
msa118713.2{361_1169NT}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD		
msa118713.2{361_CJB110}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD		

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_M781}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_18RS21}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_A909}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_COH1}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_H36B}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_JM9130013}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_M732}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{GBS361_2603}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
Consensus	*****	*****	*****	*****	*****
	701			731	
msa118713.2{361_090}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_1169NT}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_CJB110}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_M781}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_18RS21}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_A909}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_COH1}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_H36B}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_JM9130013}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_M732}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{GBS361_2603}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
Consensus	*****	*****	*****	*	

Table 76: Comparative Sequences relating to SAG0260

SEQ ID NO. 7601

STRAIN 2603

ATGAAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTAA
 AATAATATTAAATTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCTCTGGA
 GCAGGGAATCTACCTTGATTAAAACTATGCTTGGCATGAAAAAGCAGATAAGGGAACA
 GCTCTTGTCTTGATACCTCAATGCCAGATCGTAATATTTTAAATCAAATGGCTATATG
 GCTCAATCTGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTTGGA
 AAAATGAAAGGTATTCAAAAACTGAATTAACACAGCAGATAACTCATATTTCTAAAGTA
 GTAGATCTAGAAAACCACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAAAGA
 CGGCTTTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTAACTCTAGATGAACCT
 ACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAG
 GATGAAGACATTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAATTAACAAGT
 AAGGTGCACTACTATTACGTGGAACATTATTGCCCTTGATACTCCATTACATTTAAAA
 AAACAATTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7602

STRAIN 090

ATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACTGTTTTAAATAAT
 ATTAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCTC
 TGGAGCAGGGAATCTACCTTGATTAAAACTATGCTTGGCATGAAAAAG
 CAGATAAGGGAACAGCTCTTGTCTTGATACTCAAATGCCAGATCGTAAT
 ATTTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCCTTATACGAATC
 TTTAACTGCCCTTAGAAATTTATTATTCTTTGGAAAAATGAAAGGTATTCT
 AAAAACTGAATTAAACACAGCAGATAACTCATATTTCTAAAGTAGTAGAT
 CTAGAAAACCACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAA
 AAGACGGCTTTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTAA
 TCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATC
 TGGCAAGAGCTAATTAATATTAAAGGATGAAGGACGTTCTATCTTTATTAC
 AACCCACCTTATGGATGAAGCAGAAATTAACAAGTAAGGTTGCACTACTAT
 TACGTGGAACATTATTGCCCTTGATACTCCATTACATTTAAAAAAACAA
 TTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7603

STRAIN A909

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATGCCTCA
 GAAACCGTTTTAAATAATATTAAATTTGGAGGTGTTTAAAGGCGAAATAAT
 TGGATTAAATAGGACCCCTCTGGAGCAGGGAATCTACCTTGATTAAAACTA
 TGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTGATACT
 CAAATGCCAGATCATAATATTTTAAATCAAATTGGCTATATGGCTCAATC
 TGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTTG
 GAAAAATGAAAGGTATTCAAAAACTGAATTAAACACAGCAGATAACTCAT
 ATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTCTCAGG
 TTAATCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
 GAAACCCACAGTTTTAATCTAGATGAACCTACCGTTGGAATTGATCCA
 TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGAAGG
 ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAATTAACAA
 GTAAGGTTGCACTACTATTACGTGGAACATTATTGCCCTTGATACTCCA
 TTACATTTAAAAAAACAAATTTAATGTGAGTACTATTGAGGAAGTTTTCTT
 AAAAGCTGAAGGAGAA

SEQ ID NO. 7604

STRAIN H36B

AAAAAAGTCATTGATTAAAAAACTACAAAAAGCATATGCC
 TCAGAAACCGTTTTAAATAATATTAAATTTGGAGGTGTTTAAAGGCGAAAT
 AATTGGATTAAATAGGACCCCTCTGGAGCAGGGAATCTACCTTGATTAAAA
 CTATGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTGAT
 ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCA
 ATCTGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCT
 TTGAAAAATGAAAGGTATTCAAAAACTGAATTAAACACAGCAGATAACT
 CATATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTCTC
 AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
 TTGGAACCCACAGTTTTAATCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGA
 AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAATTA
 CAAGTAAGGTTGCACTACTATTACGTGGAACATTATTGCCCTTGATACT
 CCATTACATTTAAAAAAACAAATTTAATGTGAGTACTATTGAGGAAGTTTT
 CTTAAAGCTGAAGGAGAA

SEQ ID NO. 7605

STRAIN 18RS21

GATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTTAAATAA
 TATTAAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCT
 CTGGAGCAGGGAATCTACCTTGATTAAAACTATGCTTGGCATGAAAAA
 GCAGATAAGGGAACAGCTCTTGTCTTGATACTCAAATGCCAGATCGTAA
 TATTTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCCTTATACGAGT
 CTTTAACTGGCTTAGAAAAATTTATTATTCTTTGAAAAATGAAAGGTATT
 CAAAAACCTGAATTAAACACAGCAGATAACTCATATTTCTAAAGTAGTAGA
 TCTAGAAAACCACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGA
 AAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTAA
 ATCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAAT
 CTGGCAAGAGCTAATTAATATTAAAGGATGAAGGACATTTCTATCTTTATTA
 CAACCCACGTTATGGATGAAGCAGAAATTAACAAGTAAGGTTGCACTACTA

Table 76: Comparative Sequences relating to SAG0260

TTACGTGGAACATTATTGCCTTTGATACTCCATTACATTTAAAAAACA
ATTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7606

STRAIN M732

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATACGCCTCA
GAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTTAAAGGAGAAATAAT
TGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAAAACTA
TGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACT
CAAATGCCAGATCGTAATTTTAAATCAAATTGGCTATATGGCTCAATC
TGATGCCCTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTG
GAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAAATCAT
ATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTCTCAGG
TTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
GAAACCCCAAGTTTAACTCTAGATGAACCTACCGTTGGAATTGATCCA
TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGAAGG
ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAAACAA
GTAAGGTGCACTACTATTACGTGGAACATTATTGCCTTTGATACTCCA
TTACATTTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTCTT
AAAAGCTGAAGGAGAA

SEQ ID NO. 7607

STRAIN COH1

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATACGCCTCAGAA
ACITGTTTTAAATAATATTAATTTGGAGGTGTTTTAAAGGAGAAATAATTGG
ATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAAAACTATGC
TTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACTCAA
ATGCCAGATCGTAATTTTAAATCAAATTGGCTATATGGCTCAATCTGA
TGCTTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTGGA
AAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAAATCATATT
TCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTCTCAGGTTA
CTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTGGA
ACCCCAAGTTTAACTCTAGATGAACCTACCGTTGGAATTGATCCATCC
TTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGAAGGACG
TTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAAACAGTA
AGGTTGCACTACTATTACGTGGAACATTATTGCCTTTGATACTCCATTA
CATTTAAAAAACAATTTAATGTGAGTACTATTGAGGAAG

SEQ ID NO. 7608

STRAIN M781

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTTAAAGGAGA
AATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAA
AACTATGCTTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTTCTT
GATACTCAAATGCCAGATCGTAATTTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCCTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTAT
TCTTTGGAATAAGTAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATA
ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCC
TACTTGGAACCCACAGTTTAACTCTAGATGAACCTACCGTTGGAATT
GATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGA
TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
TAACAAGTAAGGTTGCACTACTATTACGTGGAACATTATTGCCTTTGAT
ACTCCATTACATTTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGT
TTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7609

STRAIN CJB110

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATG
CCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTTAAAGGCGAA
ATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAA
AACTATGCTTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTTCTTG
ATACTCAAATGCCAGATCGTAATTTTAAATCAAATTGGCTATATGGCT
CAATCTGATGCCCTTATACGAATCTTTAACTGCTTAGAAAAATTTATTATT
CTTTGGAATAAGTAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAA
CTCATATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTC
TCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCT
ACTTGGAACCCACAGTTTAACTCTAGATGAACCTACCGTTGGAATTG
ATCATCTCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGAT
GAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
AACAAGTAAGGTTGCACTACTATTACGTGGAACATTATTGCCTTTGATA
CTCCATTACATTTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTT
TTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7610

STRAIN 1169NT

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTTAAAGGCGA
AATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAA
AACTATGCTTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTTCTT
GATACTCAAATGCCAGATCGTAATTTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCCTTATACGAATCTTTAACTGCTTAGAAAAATTTATTAT

Table 76: Comparative Sequences relating to SAG0260

TCTTTGGAAAAATGAAAAGGTATTCAAAAACTGAATTAACAGCAGATA
 ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAAATTTGT
 CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCC
 TACTTGGAAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATT
 GATCCATCCTTGAGGAGAAAATCTGGCAAGAGCTAATTAATATTAAAGGA
 TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
 TAACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGAT
 ACTCCATTACATTTAAAAAAACAATTAATGTGAGTACTATTGAGGAAGT
 TTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7611

STRAIN JM9130013

AAAAAAGTCATCGATTTAAAAAACTACAAAAGCATATGCC
 TCAGAAACCGTTTAAATAATATTAAATTTGGAGGTGTTTAAAGGCGAAAT
 AATTTGGATTAATAGGACCTCTGGAGCAGGAAATCTACCTTGATTAAAA
 CTATGCTTGGCATGGAAAAGCAGATAAGGGAACAGCTCTTGTTCCTGAT
 ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTTGGCTATATGGCTCA
 ATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCT
 TTGGAATAATGAAAGGTATTCAAAAACTGAATTAACAGCAGATAAAT
 CATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAAATTTGTCTC
 AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
 TTGGAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCTTGAGGAGAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGA
 AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTA
 CAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACT
 CCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTT
 CTTAAAGCTGAAGGAGAA

PRETTY of: /biotmp/msa134270.2{*} April 10, 2003 02:14 ..

	1				50
msa134270.2{391_COH1}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_M732}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_M781}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_090}	-----	-----ATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_CJB110}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_1169NT}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_18RS21}	-----	-----gATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_2603}	atgaaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_A909}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_JM9130013}	-----aaaaaag	tcacgcgATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_H36B}	-----aaaaaag	tcattgATTT	AAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
Consensus	***-----	-----****	*****	*****	*..*****

	51				100
msa134270.2{391_COH1}	AACtGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGa	GAAATAATTG
msa134270.2{391_M732}	AACtGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGa	GAAATAATTG
msa134270.2{391_M781}	AACtGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGa	GAAATAATTG
msa134270.2{391_090}	AACtGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_CJB110}	AACtGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_1169NT}	AACtGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_18RS21}	AACcGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_2603}	AACcGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_A909}	AACcGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_JM9130013}	AACcGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_H36B}	AACcGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
Consensus	***-*****	*****	*****	*****	*****

	101				150
msa134270.2{391_COH1}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_M732}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_M781}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_090}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_CJB110}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_1169NT}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_18RS21}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_2603}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_A909}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_JM9130013}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_H36B}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
Consensus	*****	*****	*****	*****	*****

	151				200
msa134270.2{391_COH1}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_M732}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_M781}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_090}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_CJB110}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_1169NT}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_18RS21}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_2603}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_A909}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA

Table 76: Comparative Sequences relating to SAG0260

msa134270.2{391_JM9130013}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_H36B}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
Consensus	*****	*****	*****	*****	*****
	201				250
msa134270.2{391_COH1}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_M732}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_M781}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_090}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_CJB110}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_1169NT}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_18RS21}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_2603}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_A909}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_JM9130013}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_H36B}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
Consensus	*****	*-*****	*****	*****	*****
	251				300
msa134270.2{391_COH1}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_M732}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_M781}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_090}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_CJB110}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_1169NT}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_18RS21}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_2603}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_A909}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_JM9130013}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_H36B}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
Consensus	*****-*	***-*****	****-*****	*****	*****
	301				350
msa134270.2{391_COH1}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_M732}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_M781}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_090}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_CJB110}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_1169NT}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_18RS21}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_2603}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_A909}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_JM9130013}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_H36B}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
Consensus	*****	*****	*****	*****	*****
	351				400
msa134270.2{391_COH1}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_M732}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_M781}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_090}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_CJB110}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_1169NT}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_18RS21}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_2603}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_A909}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_JM9130013}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_H36B}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
Consensus	*****	*****	*****	*****	*****
	401				450
msa134270.2{391_COH1}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_M732}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_M781}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_090}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_CJB110}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_1169NT}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_18RS21}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_2603}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_A909}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_JM9130013}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_H36B}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
Consensus	*****	*****	*****	*****	*****
	451				500
msa134270.2{391_COH1}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_M732}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_M781}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_090}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_CJB110}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_1169NT}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_18RS21}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_2603}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC

Table 76: Comparative Sequences relating to SAG0260

msa134270.2{391_A909}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_JM9130013}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_H36B}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_M732}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_M781}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_090}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_CJB110}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_1169NT}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_18RS21}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_2603}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_A909}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_JM9130013}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_H36B}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_M732}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_M781}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_090}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_CJB110}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_1169NT}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_18RS21}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_2603}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_A909}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_JM9130013}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_H36B}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_M732}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_M781}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_090}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_CJB110}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_1169NT}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_18RS21}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_2603}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_A909}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_JM9130013}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_H36B}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	G-----
msa134270.2{391_M732}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_M781}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_090}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_CJB110}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_1169NT}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_18RS21}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_2603}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_A909}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_JM9130013}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_H36B}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	AAGCTGAAGG	AGAA			
msa134270.2{391_M732}	AAGCTGAAGG	AGAA			
msa134270.2{391_M781}	AAGCTGAAGG	AGAA			
msa134270.2{391_090}	AAGCTGAAGG	AGAA			
msa134270.2{391_CJB110}	AAGCTGAAGG	AGAA			
msa134270.2{391_1169NT}	AAGCTGAAGG	AGAA			
msa134270.2{391_18RS21}	AAGCTGAAGG	AGAA			
msa134270.2{391_2603}	AAGCTGAAGG	AGAA			
msa134270.2{391_A909}	AAGCTGAAGG	AGAA			
msa134270.2{391_JM9130013}	AAGCTGAAGG	AGAA			
msa134270.2{391_H36B}	AAGCTGAAGG	AGAA			
Consensus	*****	****			

SEQ ID NO. 7612

STRAIN 2603 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVPKGEIIGLIGPSGAGKSTLIKMLGMEKADKGTALVLDTPMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKVVDLENQLDKFVSGSYSGMKRRSLALALLGNPTVLILDEPTVGIDPSLRRIKWQELINKDEGHSIFITTHVMDAEITSKVALLLRGNI AFDTPLHLKQFNV

SEQ ID NO. 7613

Table 76: Comparative Sequences relating to SAG0260

STRAIN 090 frame: 3
 LKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTALVLD
 QMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQIITHISKVVDLENQ
 LDKFVSGYSGGKMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKDEGRSI
 FITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7614

STRAIN A909 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGKMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7615

STRAIN H36B frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGKMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7616

STRAIN 18RS21 frame: 1
 DLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTALVLD
 TQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKVVDLEN
 QLDKFVSGYSGGKMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKDEGHS
 IFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7617

STRAIN M732 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGKMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7618

STRAIN COH1 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGKMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7619

STRAIN M781 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGKMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7620

STRAIN CJB110 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGKMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7621

STRAIN 1169NT frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGKMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7622

STRAIN JM9130013 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGKMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

PRETTY of: /biotmp/msa134470.2{*} April 10, 2003 02:16 ..

	1		50
msa134470.2{391_090}	-----LKKLQ	KAYASETVLN	NINLEVFKEG IIGLIGPSGA GKSTLIKTM
msa134470.2{391_1169NT}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKEG IIGLIGPSGA GKSTLIKTM
msa134470.2{391_CJB110}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKEG IIGLIGPSGA GKSTLIKTM
msa134470.2{391_COH1}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKEG IIGLIGPSGA GKSTLIKTM
msa134470.2{391_M732}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKEG IIGLIGPSGA GKSTLIKTM
msa134470.2{391_M781}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKEG IIGLIGPSGA GKSTLIKTM
msa134470.2{391_18RS21}	----DLKKLQ	KAYASETVLN	NINLEVFKEG IIGLIGPSGA GKSTLIKTM
msa134470.2{391_2603}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKEG IIGLIGPSGA GKSTLIKTM
msa134470.2{391_H36B}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKEG IIGLIGPSGA GKSTLIKTM
msa134470.2{391_JM9130013}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKEG IIGLIGPSGA GKSTLIKTM

Table 76: Comparative Sequences relating to SAG0260

msa134470.2{391_A909}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKE	IIGLIGPSGA	GKSTLIKTML
Consensus	*****	*****	*****	*****	*****
	51				100
msa134470.2{391_090}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_1169NT}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_CJB110}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_COH1}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_M732}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_M781}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_18RS21}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_2603}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_H36B}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_JM9130013}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_A909}	GMEKADKGTA	LVLDTQMPDh	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
Consensus	*****	*****	*****	*****	*****
	101				150
msa134470.2{391_090}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_1169NT}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_CJB110}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_COH1}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_M732}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_M781}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_18RS21}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_2603}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_H36B}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_JM9130013}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_A909}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
Consensus	*****	*****	*****	*****	*****
	151				200
msa134470.2{391_090}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_1169NT}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_CJB110}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_COH1}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_M732}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_M781}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_18RS21}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGhSIFITTH	VMDEAELTSK
msa134470.2{391_2603}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGhSIFITTH	VMDEAELTSK
msa134470.2{391_H36B}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_JM9130013}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_A909}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
Consensus	*****	*****	*****	*****	*****
	201		224		
msa134470.2{391_090}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_1169NT}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_CJB110}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_COH1}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_M732}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_M781}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_18RS21}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_2603}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_H36B}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_JM9130013}	VALLLRGNII	AFDTPHLKK	QFNV		
msa134470.2{391_A909}	VALLLRGNII	AFDTPHLKK	QFNV		
Consensus	*****	*****	****		

Table 77: Comparative Sequences relating to SAG2059

SEQ ID NO. 7701

STRAIN 2603

TTGCCTATGTTGCTCTGTTGGTTTAGTTTTAGAGGGTGGCGGAATGAGAGGTCTTTATACT
GCTGGAGTTTTAGATGCTTTTCTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTC
TCTGCTGCTGTCATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
TACAATAAAAAAGTATTATCCACCCTAAATATATGAGTCTAAGGTCATGGTTTCGAACA
GGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTATGAAATGGATGTATTT
GACGATGAAGCATTTAAAAAATCAAGTATTGATTTTTACGTAGTTGCTACAGAGATGACA
TCTGGTAAACCTGAATATTTTAAATTTGATAGTGTTTTTGAACAAATGGAATTTTACGT
GCTAGTTTCAAGATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGATTGACAAG
TTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTCAAGTGGACGATTG
TATAAACTCTGTATAGGAAATATCCTAATTTTGTAAAGACAGCCTCGAATCGGTACCAA
CAGTATAATAATAGTCTTGAAAAGGTCTGAGCCTTGAAAAACAGGCGATCTATTTGCA
ATTAGACCGAGTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAATAGTTAT
CTAATGAAA

SEQ ID NO. 7702

STRAIN 090

CCTATGTTGTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
CTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGCTCTGCTGGTGC
ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAAGTATTTATCCACCCTAAATATATGAGTCTAAGGTCATGG
TTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
TATGAAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
AAAATTGATAGTGTTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGC
ATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
GCCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
TTGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAA
AAGGTCTAGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7703

STRAIN A909

CCTATGTTGTCTGTTGGTTTAGTTTTAGAG
GGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTTCT
AGATGCAGGAATAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGCAT
TGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
AATAAAAAAGTATTTATCCACCCTAAATATATGAGTCTAAGGTCATGGCT
TCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTA
TGAAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGAT
TTTTACGAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
AATTGATAGTGTTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGCAT
TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
GGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGATT
TGACAAGTTGATTTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
CTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
GTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAAA
GGTCATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
TAGTTATCTAATGAAA

SEQ ID NO. 7704

STRAIN H36B

CCTATGTTGTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
CTAGATGCAGGAATAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGC
ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAAGTATTTATCCACCCTAAATATATGAGTCTAAGGTCATGG
CTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTA
TATGAAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTACGAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTT
AAAATTGATAGTGTTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGC
ATTACAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
GCCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
TTGTAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAA
AAGGTCTAGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCAAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7705

Table 77: Comparative Sequences relating to SAG2059

STRAIN 18RS21

CCTATGTTGTCTGTTGGTTTAGTTTAGAGG
 GTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTATAGATGCTTTTCTA
 GATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTGCAIT
 GTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACA
 ATAAAAAGTATTTATCCCAACCCTAAATATATGAGTCTAAGGTCATGGTTT
 CGAACAGGGAATTTTGTAAATAAGATTTACCTATTATGAAGTTCCTAT
 GAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGATT
 TTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAA
 ATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTACGACATT
 ACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATG
 GTGGTTTATCTGATAGTATTTCCCGTTGATTGTTGCCCGTGGTTTAGGATTT
 GACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCC
 TTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTG
 TAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAAAG
 GTCATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGAGTAA
 GAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGTA
 TTTATCAGCTTGGTATGAAAAGATGCTAAAAGTGTGATGCCTGAGCTGAAT
 AGTTATCTAATGAAA

SEQ ID NO. 7706

STRAIN M732

CCTATGTTGTCTGTTGGTTTAGTTTAGA
 GGGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTATAGATGCTTTTC
 TAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCA
 TTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATA
 CAATAAAAAGTATTTATCCCAACCCTGAATATAAGTCTAAGATCATGGC
 TTCGAACAGGGAATTTTGTAAATAAGATTTACCTATTATGAAGTTCCT
 ATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGA
 TTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTA
 AAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTACGCA
 TTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGA
 TGGTGGTTTATCTGATAGTATTTCCCGTTGATTGTTGCCCGTGGTTTAGGAT
 TTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAG
 CCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTT
 TGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAA
 AGGTATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGAGT
 AAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAG
 TATTATCAGCTTGGTATGAAAATATGCTAAAAGTGTGATGCCTGAGCTGA
 ATAGTTATCTAATGAAA

SEQ ID NO. 7707

STRAIN COH1

CCTATGTTGTCTGTTGGTTTAGTTTAA
 GAGGGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTATAGATGCTTT
 TCTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTG
 CATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
 TACATAAAAAGTATTTATCCCAACCCTGAATATATGAGTCTAAGATCATG
 GCTTCGAACAGGGAATTTTGTAAATAAGATTTACCTATTATGAAGTTC
 CTATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATT
 GATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
 TAAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTACG
 CATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
 GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTGTTGCCCGTGGTTTAGG
 ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
 AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
 TTTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAAGTATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGA
 GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 AGTATTTATCAGCTTGGTATGAAAATATGCTAAAAGTGTGATGCCTGAGCT
 GAATAGTTATCTAATGAAA

SEQ ID NO. 7708

STRAIN M781

CCTATGTTGTCTGTTGGTTTAGTTTAG
 AGGGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTATAGATGCTTTT
 CTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGC
 ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
 ACAATAAAAAGTATTTATCCCAACCCTGAATATAAGTCTAAGATCATGG
 CTTTGAACAGGGAATTTTGTAAATAAGATTTACCTATTATGAAGTTC
 TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
 ATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
 AAAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTACG
 ATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
 ATGGTGGTTTATCTGATAGTATTTCCCGTTGATTGTTGCCCGTGGTTTAGGA
 TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
 GCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
 TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAAGTATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGA
 GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 GTATTTATCAGCTTGGTATGAAAATATGCTAAAAGTGTGATGCCTGAGCTG
 AATAGTTATCTAATGAAA

Table 77: Comparative Sequences relating toSAG2059

SEQ ID NO. 7709

STRAIN CJB110

CCTATGTTGTCGTGGTTTGTAGTTTAA
 GAGGGTGGCGGAATGAGAGGTCCTTATACCTGCTGGAGTTTGTAGATGCTTT
 TCTAGATGCAGGAATAAAATAGATGGTATCGTATCTGTCTCTGCTGGTG
 CATTTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
 TACAATAAAAAGTATTTATCCACCCCTAAATATATGAGTCTAAGGTCATG
 GTTTCGAACAGGGAATTTTGTAAATAAGATTTCACCTATTATGAAGTTC
 CTATGAAATTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATT
 GATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
 TAAATTTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAG
 CATACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
 GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGG
 ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
 AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
 TTTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCGA
 GTAAGAGCTTGGTTATTTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCCTGAGCT
 GAATAGTTATCTAATGAAA

SEQ ID NO. 7710

STRAIN 1169NT

CCTATGTTGTCGTGGTTTGTAGTTTGTAGGGTG
 GCGGAATGAGAGGTCCTTATACCTGCTGGAGTTTGTAGATGCTTTTCTAGAT
 GCAGGAATAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCATTGTT
 TGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAACAATA
 AAAAGTATTTATCCACCCCTAAATATATGAGTCTAAGATCATGGCTTCGA
 ACAGGGAATTTTGTAAATAAGATTTCACCTATTATGAAGTTCCCTATGAA
 ATTTGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATTGATTTT
 ACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAATTT
 GATAGTGTCTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAGCAATTACC
 AGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATGGTG
 GTTTATCTGATAGTATCCCGTTGATTTTGCCCGTGGTTTAGGATTTGAC
 AAGTTGATTTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTTC
 AAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTGTAA
 AGACAGCCTCGAATCGGTACCAACAGTATAATAATAGCCTTGAAAAGGTC
 ATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGGCCGAGTAAAAAG
 CTTGGTTATTGTCGGCTTAGAGAAGAATCCGGATAAACTTGATAGTATTT
 ATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCCTGAGCTGAATAGT
 TATCTAATGAAA

SEQ ID NO. 7711

STRAIN JM9130013

CCTATGTTGTCGTGGTTTGTAGTTTGTAGAG
 GGTGGCGGAATGAGAGGTCCTTATACCTGCTGGAGTTTGTAGATGCTTTTCT
 AGATGCAGGAATAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGCA
 TGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
 AATAAAAAGTATTTATCCACCCCTAAATATATGAGTCTAAGGTCATGGCT
 TCGAACAGGGAATTTTGTAAATAAGATTTCACCTATTATGAAGTTCCCTA
 TGAAATTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATTGAT
 TTTTACGCGATTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
 AATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAGCAT
 TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
 GGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGATT
 TGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
 CTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
 GTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAAA
 GGTATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
 AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
 ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCCTGAGCTGAA
 TAGTTATCTAATGAAA

PRETTY of: /biotmp/msa47199.2{*} February 19, 2003 05:51 ..

	1		50
msa47199.2{394_A909}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_H36B}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_JM9130013}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_090}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_18RS21}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_2603}	ttgCCTATGT	TGTCGTGGTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_CJB110}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_COH1}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_M732}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_M781}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_1169NT}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
Consensus	*****	*****	*****
	51		100
msa47199.2{394_A909}	TCCTTATACT	GCTGGAGTTT	TAGATGCTTT TCTAGATGCA GGAATAAAAG
msa47199.2{394_H36B}	TCCTTATACT	GCTGGAGTTT	TAGATGCTTT TCTAGATGCA GGAATAAAAG
msa47199.2{394_JM9130013}	TCCTTATACT	GCTGGAGTTT	TAGATGCTTT TCTAGATGCA GGAATAAAAG

Table 77: Comparative Sequences relating toSAG2059

msa47199.2{394_090}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_18RS21}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_2603}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_CJB110}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_COH1}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_M732}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_M781}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_1169NT}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_H36B}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_JM9130013}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_090}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_18RS21}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_2603}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_CJB110}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_COH1}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_M732}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_M781}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
msa47199.2{394_1169NT}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATTTT
Consensus	*****	*-*****	*****	*****	*****
msa47199.2{394_A909}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_H36B}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_JM9130013}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_090}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_18RS21}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_2603}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_CJB110}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_COH1}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_M732}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_M781}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
msa47199.2{394_1169NT}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTATC
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_H36B}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_JM9130013}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_090}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_18RS21}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_2603}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_CJB110}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_COH1}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_M732}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_M781}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_1169NT}	CCACCCTaAA	TATATGAGTC	TAAGaTCATG	GcTTcGAACA	GGGAATTTTG
Consensus	*****-*	*****	*****	*-*****	*****
msa47199.2{394_A909}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_H36B}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_JM9130013}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_090}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_18RS21}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_2603}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_CJB110}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_COH1}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_M732}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_M781}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_1169NT}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_H36B}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_JM9130013}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_090}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_18RS21}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_2603}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_CJB110}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_COH1}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_M732}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_M781}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_1169NT}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
Consensus	*****	*****	*****	*****	-*****
msa47199.2{394_A909}	AGAGATGACA	TCGGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_H36B}	AGAGATGACA	TCGGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG

Table 77: Comparative Sequences relating toSAG2059

msa47199.2{394_JM9130013}	AGAGATGACA	TCTGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_090}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_18RS21}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_2603}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_CJB110}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_COH1}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_M732}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_M781}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_1169NT}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
Consensus	*****	*****	*****	*****	*****
401					
msa47199.2{394_A909}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_H36B}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_JM9130013}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_090}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_18RS21}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_2603}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_CJB110}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_COH1}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_M732}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_M781}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_1169NT}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
Consensus	*****	*****	*****	*****	*****
451					
msa47199.2{394_A909}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_H36B}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_JM9130013}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_090}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_18RS21}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_2603}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_CJB110}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_COH1}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_M732}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_M781}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_1169NT}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
Consensus	*****	*****	*****	*****	*****
501					
msa47199.2{394_A909}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_H36B}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_JM9130013}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_090}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_18RS21}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_2603}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_CJB110}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_COH1}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_M732}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_M781}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_1169NT}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
Consensus	***-*****	*****	*****	*****	*****
551					
msa47199.2{394_A909}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_H36B}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_JM9130013}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_090}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_18RS21}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_2603}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_CJB110}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_COH1}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_M732}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_M781}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_1169NT}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
Consensus	*****	*****	*****	*****	*****
601					
msa47199.2{394_A909}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_H36B}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_JM9130013}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_090}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_18RS21}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_2603}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_CJB110}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_COH1}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_M732}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_M781}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_1169NT}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
Consensus	*****	*****	*****	*****	*****
651					
msa47199.2{394_A909}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA

Table 77: Comparative Sequences relating to SAG2059

msa47199.2{394_H36B}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_JM9130013}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_090}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_18RS21}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_2603}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_CJB110}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_COH1}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_M732}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_M781}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_1169NT}	tCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
Consensus	*****	*****	****-****	*****	*****
msa47199.2{394_A909}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_H36B}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_JM9130013}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_090}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_18RS21}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_2603}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_CJB110}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_COH1}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_M732}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_M781}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_1169NT}	AAACAGGCGA	TCTATTTGCA	ATTAGgCCgA	GTAAaAGCTT	GGTTATTGtC
Consensus	*****	*****	*****-*-*	*****	*****-*
msa47199.2{394_A909}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_H36B}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_JM9130013}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_090}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_18RS21}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_2603}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_CJB110}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_COH1}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_M732}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_M781}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_1169NT}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	GAAAGATGCT	AAAAGTGgGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_H36B}	GAAAGATGCT	AAAAGTGgGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_JM9130013}	GAAAGATGCT	AAAAGTGgGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_090}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_18RS21}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_2603}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_CJB110}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_COH1}	GAAAtATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_M732}	GAAAtATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_M781}	GAAAtATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_1169NT}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
Consensus	****-*****	*****-*	*****	*****	*****

SEQ ID NO. 7712

STRAIN 2603 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMSLRSWRTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYVVAATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IIVMTIRPLNYQKKPSSGRLYKTYLRKYPNFVKTASNRYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSMPELNSYLMK

SEQ ID NO. 7713

STRAIN 090 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMSLRSWRTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYVVAATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IIVMTIRPLNYQKKPSSGRLYKTYLRKYPNFVKTASNRYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSMPELNSYLMK

SEQ ID NO. 7714

STRAIN A909 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIIISVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMSLRSWRTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYAVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IIVMTIRPLNYQKKPSSGRLYKTYLRKYPNFVKTASNRYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSMPELNSYLMK

SEQ ID NO. 7715

STRAIN H36B frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIIISVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMSLRSWRTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYAVATEMTS

Table 77: Comparative Sequences relating to SAG2059

GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKCYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7716

STRAIN 18RS21 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERARLY
 NKKYLSPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVATMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKCYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7717

STRAIN M732 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERARLY
 NKKYLSPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVATMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKCYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7718

STRAIN COH1 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERARLY
 NKKYLSPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVATMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKCYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7719

STRAIN M781 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERARLY
 NKKYLSPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVATMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKCYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7720

STRAIN CJB110 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERARLY
 NKKYLSPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVATMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKCYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7721

STRAIN JM9130013 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIISVSAGALFGVNFVSRQRERARLY
 NKKYLSPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVATMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKCYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7722

STRAIN 1169NT frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERARLY
 NKKYLSPKYMMSLRSLWRTGNFVNKDFTYEVPKMLDVFDDFAFKSSIDFYVATMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKCYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

	1		50
msa47322.2{394_A909}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKVDGIISVS AGALFGVNFV
msa47322.2{394_H36B}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKVDGIISVS AGALFGVNFV
msa47322.2{394_JM9130013}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKVDGIISVS AGALFGVNFV
msa47322.2{394_090}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIVSVS AGALFGVNFV
msa47322.2{394_1169NT}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIVSVS AGALFGVNFV
msa47322.2{394_18RS21}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIVSVS AGALFGVNFV
msa47322.2{394_2603}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIVSVS AGALFGVNFV
msa47322.2{394_CJB110}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIVSVS AGALFGVNFV
msa47322.2{394_COH1}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIVSVS AGALFGVNFV
msa47322.2{394_M732}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIVSVS AGALFGVNFV
msa47322.2{394_M781}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG IKIDGIVSVS AGALFGVNFV
Consensus	*****	*****	*****
	51		100
msa47322.2{394_A909}	SRQRERARLY	NKKYLSPKYP	MSLRSLWRTG NFNKDFTYE EVPMKLDVFD
msa47322.2{394_H36B}	SRQRERARLY	NKKYLSPKYP	MSLRSLWRTG NFNKDFTYE EVPMKLDVFD
msa47322.2{394_JM9130013}	SRQRERARLY	NKKYLSPKYP	MSLRSLWRTG NFNKDFTYE EVPMKLDVFD
msa47322.2{394_090}	SRQRERARLY	NKKYLSPKYP	MSLRSLWRTG NFNKDFTYE EVPMKLDVFD
msa47322.2{394_1169NT}	SRQRERARLY	NKKYLSPKYP	MSLRSLWRTG NFNKDFTYE EVPMKLDVFD
msa47322.2{394_18RS21}	SRQRERARLY	NKKYLSPKYP	MSLRSLWRTG NFNKDFTYE EVPMKLDVFD

Table 77: Comparative Sequences relating to SAG2059

msa47322.2{394_2603}	SRQRERALRY	NKKYLSHPkY	MSLRSWfRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_CJB110}	SRQRERALRY	NKKYLSHPkY	MSLRSWfRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_COH1}	SRQRERALRY	NKKYLSHPeY	MSLRSWlRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_M732}	SRQRERALRY	NKKYLSHPeY	MSLRSWlRTG	NFVNKDFTYY	EVPMKLDVFD
msa47322.2{394_M781}	SRQRERALRY	NKKYLSHPeY	MSLRSWlRTG	NFVNKDFTYY	EVPMKLDVFD
Consensus	*****	*****-*	*****-***	*****	*****
msa47322.2{394_A909}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_H36B}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_JM9130013}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_090}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_1169NT}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_18RS21}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_2603}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_CJB110}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_COH1}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_M732}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_M781}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
Consensus	*****	***-*****	*****	*****	*****
msa47322.2{394_A909}	VvWQGGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_H36B}	VvWQGGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_JM9130013}	VvWQGGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_090}	VdWQGGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_1169NT}	VdWQGGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_18RS21}	VdWQGGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_2603}	VdWQGGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_CJB110}	VdWQGGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_COH1}	VdWQGGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_M732}	VdWQGGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_M781}	VdWQGGKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
Consensus	*-*****	*****	*****	*****	*****
msa47322.2{394_A909}	KTLYRKYPNF	VKTASNRYQQ	YNNLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_H36B}	KTLYRKYPNF	VKTASNRYQQ	YNNLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_JM9130013}	KTLYRKYPNF	VKTASNRYQQ	YNNLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_090}	KTLYRKYPNF	VKTASNRYQQ	YNNLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_1169NT}	KTLYRKYPNF	VKTASNRYQQ	YNNLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_18RS21}	KTLYRKYPNF	VKTASNRYQQ	YNNLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_2603}	KTLYRKYPNF	VKTASNRYQQ	YNNLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_CJB110}	KTLYRKYPNF	VKTASNRYQQ	YNNLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_COH1}	KTLYRKYPNF	VKTASNRYQQ	YNNLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_M732}	KTLYRKYPNF	VKTASNRYQQ	YNNLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_M781}	KTLYRKYPNF	VKTASNRYQQ	YNNLEKVMS	LEKTGDLFAI	RPSKSLVIGR
Consensus	*****	*****	*****	*****	*****-*
msa47322.2{394_A909}	LEKNPDKLDS	IYQLGMKdAK	SgMPELNSYL	MK	
msa47322.2{394_H36B}	LEKNPDKLDS	IYQLGMKdAK	SgMPELNSYL	MK	
msa47322.2{394_JM9130013}	LEKNPDKLDS	IYQLGMKdAK	SgMPELNSYL	MK	
msa47322.2{394_090}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_1169NT}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_18RS21}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_2603}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_CJB110}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_COH1}	LEKNPDKLDS	IYQLGMKyAK	SvMPELNSYL	MK	
msa47322.2{394_M732}	LEKNPDKLDS	IYQLGMKyAK	SvMPELNSYL	MK	
msa47322.2{394_M781}	LEKNPDKLDS	IYQLGMKyAK	SvMPELNSYL	MK	
Consensus	*****	*****-*	*-*****	**	

Table 78: Comparative Sequences relating to SAG1016

SEQ ID NO. 7801

STRAIN 2603

ATGAAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAACGAATTAATTTACCTTCTT
 AATAAGATGATTTCTAACCTCGTTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCT
 ATTTTACTTAGAGAACTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCT
 GGGTTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCACCATTTATGATATTTGCG
 ACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGATTATTTGTTA
 AAACCCCTATGATTTTGATAGGCTAAAGCAAGCTATGGATAGAGTAAAGGAGCGCTAAGT
 ACATCTCAATTTATAGAGAGCGTAACCTCCGGTCTCTCTTCAAGCAACAGTATCCATTG
 ACAGTAGAAGATCGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATG
 CAAGGAAAACTGATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTCTCTACAA
 CAATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTACATCGCTCTTACATTGTG
 AACATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCAACACTTCAGTTACACCTT
 TGTATAAAATAACAGTTCCTGTTAGCAGAGCAATGTAAACCCCTAAACAAATGTTA
 GGCATATCTACC

SEQ ID NO. 7802

STRAIN 090

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAA
 CGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
 AGGCGCATGATATGGCTACTGCAATAGCTATTTTACTTAGAGAACTTTT
 GATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATT
 AGCAGAGTATATCAATAAAATGCCAAACCACCATTTATGATATTTGCGA
 CTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGAT
 TATTTGTAAACCCCTATGATTTTGATAGGCTAAAGCAAGCTATGGATAG
 AGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCG
 GTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTAT
 CTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACT
 GATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTCTCTACAAC
 AATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTACATCGCTCT
 TACATTGTGAACATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCA
 AACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAG
 CAAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7803

STRAIN A909

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAA
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GCGCATGATATGGCTACTGCAATAGCTATTTTACTTAGAGAACTTTT
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCACCATTTATGATATTTGCGAC
 TGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCGG
 CCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG
 ATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTCTCTACAACA
 ATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTGACCGCTCTT
 ACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCA
 ACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAGC
 AAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7804

STRAIN H36B

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGT
 AACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGC
 AGAGGCGCATGATATGGCTACTGCAATAGCTATTTTACTTAGAGAACTTT
 TTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAA
 TTAGCAGAGTATATCAATAAAATGCCAAACCACCATTTATGATATTTGCG
 GACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTG
 ATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAGCTATGGAT
 AGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTTC
 CGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCT
 ATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAA
 CTGATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTCTCTACA
 ACAATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTGACCGCT
 CTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGGTTTAAAC
 CAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAG
 AGCAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7805

STRAIN 18RS21

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAA
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GCGCATGATATGGCTACTGCAATAGCTATTTTACTTAGAGAACTTTT
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCACCATTTATGATATTTGCGAC
 TGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAACCCCTATGATTTTGATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCGG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG

Table 78: Comparative Sequences relating to SAG1016

ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
 ACATTTGTGAACATTAAATGCTATTAAAAACGATTGAACCTTGGTTTAAACCAA
 ACATTTGAGTTACACCTTTGTAATAAAATAACAGTTCTCTGTTAGCAGAGC
 AAATGTAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7806

STRAIN M732

AAAGTTTTAGTAGTTGATGATGAACCAAGTT
 GCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGT
 TATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAG
 AAATTTTGTAGTAGCCTGTTAGATATCCATCTCAGAGATGATTCTGGG
 TTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCAACATTATTGAT
 ATTCGCGACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCAGGATG
 CGCGTATTAATTTGTTAAACCCCTATGAGTTTGTAGGTTAAAGCAAGCT
 ATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGT
 AGCTTCCGGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATC
 GAATCTATCTGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCAA
 GGAAAACTGATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTC
 TCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTAC
 ATCGCTCTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGG
 TTTAACCAACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCTCTGT
 TAGCAGAGCAATGTAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7807

STRAIN COH1

AAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTA
 ACCAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCA
 GAGGCGCATGATATGGCTACTGCTATTAGCTATTTTACTTAGAGAACTTT
 TGATGTAGCCTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAAT
 TAGCAGAGTATATCAATAAAATGCCAAACCAACATTATTGATATTCGCG
 ACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCAGGATGCGCGTGA
 TTATTTGTTAAACCCCTATGAGTTTGTAGGTTAAAGCAAGCTATGGATA
 GAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCC
 GGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTA
 TCTGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCAAGGAAAC
 TGATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTCTCTACAA
 CAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTC
 TTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGGTTTAAACC
 AAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCTCTGTTAGCAGA
 GCAATGTAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7808

STRAIN M781

AAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTAAC
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GGGCGCATGATATGGCTACTGCTATTAGCTATTTTACTTAGAGAACTTTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCAACATTATTGATATTCGCGAC
 TGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCAGGATGCGCGTGATT
 ATTTGTTAAAAACCCCTATGAGTTTGTAGGTTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCCGG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCAAGGAAACCTG
 ATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
 ACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCAA
 ACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCTCTGTTAGCAGAGC
 AAATGTAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7809

STRAIN CJB110

CTTAATAAGTATGATTCTAACCTCGTTATAGCAGAGGCGCATGATATGGC
 TACTGCATTAGCTATTTTACTTAGAGAACTTTTGATGTAGCACTGTTAG
 ATATCCATCTCAGAGATGATTCTGGGTTGCAATTAGCAGAGTATATCAAT
 AAAATGCCAAACCAACATTATTGATATTCGCGACTGCTTATGATCAATA
 TGCTATTCAAGCTTTTGAGCATGATGCGCGTGATTATTGTTAAAAACCT
 ATGAGTTTGTAGGCTAAAGCAAGTATGGATAGAGTAAAGGAGCGCTA
 AGTACATCTACAATTATAGAGAGCGTAACTTCCGGCCCTCTCTCAAGCA
 ACAGTATCCATTGACAGTAGAAGATGAAATCTATCTGGTGTGCGCGGATG
 ATATCTCTTTTGATTGAAGCTATGCAAGGAAACCTGATTATACAAACACCT
 GATAAAAAATTATGAAATTGATGGCTCTCTACAACAATGGCAAGATAAACT
 ACCATCATCTCAATTTGTACGGGTGCAACCGCTCTTACATTGTGAATATTA
 ATGCTATTAACGAGATTGAACCTTGGTTTAAACCAACACTTCAGTTACAC
 CTTTGTAAATAAAATAACAGTTCTCTGTTAGCAGAGCAATGTAAACCCCT
 AAAACAAATGTTAGG

SEQ ID NO. 7810

STRAIN 1169NT

AAAGTTTTAGTAGTTGATGATGAACCAAG
 TTGCACGTAACGAATTAATTTATCTTCTTAATAAGTATGATTCTAACCTC
 GTTATAGCAGAGGCGCATGATATAGCTACTGCATTAGCTATTTTACTTAG

Table 78: Comparative Sequences relating to SAG1016

AGAAACTTTTGTAGTACTGTTAGATATCCATCTCAGAGATGATTCTG
GGTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACTATTG
ATATTCCGCACTGCTTATGATCAATATGCTATTTCAGGCTTTGAGCATGA
TGCCTGTGATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAG
CTATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGC
GTAACCTCCGCCCCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAGA
TCGAATCTATCTGGTTCGGCGGATGATATCCTTTTGATTGAAGCTATGC
AAGGAAAACGTATTATACAAACACCTGATAAAAATTATGAAATTGATGGC
TCTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGT
GCACCGCTCTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTT
GGTTTAAACCAACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCTC
GTTAGCAGAGCAAATGTAAACCCCTAAACAAATGTTAGGCATATCTAC
C

SEQ ID NO. 7811

STRAIN JM9130013

AAAGTTTGTAGTGTAGTGAACCACT

TGCACGTAAACGAATTAATTACCTTCTTAATAAGTATGATTCTAACCTCG
TTATAGCAGAGGCGCATGATATGGCTACTGCAATTAGCTATTTTACTTAGA
GAAACTTTTGTAGTACTGTTAGATATCCATCTCAGAGATGATTCTGG
GTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACTATTGTA
TATTCCGCACTGCTTATGATCAATATGCTATTCAAGCTTTTGTAGCATGAT
GCGCGTGTATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAGC
TATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCG
TAACCTCCGCCCCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAGAT
CGAATCTATCTGGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGCA
AGGAAAACGTATTATACAAACACCTGATAAAAATTATGAAATTGATGGCT
CTCTACACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTG
CACCGCTCTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTG
GTTTAAACCAACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCTC
TTAGCAGAGCAAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa141507.2{*} April 10, 2003 06:36 ..

	1		50
msa141507.2{399_A909}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_CJB110}	-----	-----	-----
msa141507.2{399_H36B}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_JM9130013}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_1169NT}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_090}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_18RS21}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_2603}	atgaaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_COH1}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_M732}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_M781}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
Consensus	***-----	-----	-----
	51		100
msa141507.2{399_A909}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_CJB110}	-----CTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_H36B}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_JM9130013}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_1169NT}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_090}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_18RS21}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_2603}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_COH1}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_M732}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_M781}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
Consensus	-----***	*****	*****
	101		150
msa141507.2{399_A909}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_CJB110}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_H36B}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_JM9130013}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_1169NT}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_090}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_18RS21}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_2603}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_COH1}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_M732}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_M781}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
Consensus	*****	*****	*****
	151		200
msa141507.2{399_A909}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA
msa141507.2{399_CJB110}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA
msa141507.2{399_H36B}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA
msa141507.2{399_JM9130013}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA
msa141507.2{399_1169NT}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA

Table 78: Comparative Sequences relating to SAG1016

msa141507.2{399_090}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_18RS21}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_2603}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_COH1}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_M732}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_M781}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCCTATG
msa141507.2{399_CJB110}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCCTATG
msa141507.2{399_H36B}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCCTATG
msa141507.2{399_JM9130013}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCCTATG
msa141507.2{399_1169NT}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCCTATG
msa141507.2{399_090}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCCTATG
msa141507.2{399_18RS21}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCCTATG
msa141507.2{399_2603}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCCTATG
msa141507.2{399_COH1}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCCTATG
msa141507.2{399_M732}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCCTATG
msa141507.2{399_M781}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCCTATG
Consensus	*****	*****	*****	*****-***	*****
msa141507.2{399_A909}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_CJB110}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_H36B}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_JM9130013}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_1169NT}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_090}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_18RS21}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_2603}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_COH1}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_M732}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_M781}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
Consensus	*****	*****-***	*****-*	*****	*****
msa141507.2{399_A909}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_CJB110}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GnTATGGATA	GAGTAAAGG
msa141507.2{399_H36B}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_JM9130013}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_1169NT}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_090}	AAACCCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_18RS21}	AAACCCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_2603}	AAACCCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_COH1}	AAACCCCTATG	AgTTTGATAG	GtTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_M732}	AAACCCCTATG	AgTTTGATAG	GtTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_M781}	AAACCCCTATG	AgTTTGATAG	GtTAAAGCAA	GcTATGGATA	GAGTAAAGG
Consensus	*****	*-*****	*-*****	*-*****	*****
msa141507.2{399_A909}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_CJB110}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_H36B}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_JM9130013}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_1169NT}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_090}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_18RS21}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_2603}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_COH1}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_M732}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_M781}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_CJB110}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATnGAATCTA	TCTGGTGTCTG
msa141507.2{399_H36B}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_JM9130013}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_1169NT}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_090}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_18RS21}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_2603}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_COH1}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_M732}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_M781}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
Consensus	*****	*****	*****	**-*****	*****
msa141507.2{399_A909}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_CJB110}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_H36B}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_JM9130013}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA

Table 78: Comparative Sequences relating to SAG1016

msa141507.2{399_1169NT}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_090}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_18RS21}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_2603}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_COH1}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_M732}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_M781}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_CJB110}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_H36B}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_JM9130013}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_1169NT}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_090}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_18RS21}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_2603}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_COH1}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_M732}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_M781}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_CJB110}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_H36B}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_JM9130013}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_1169NT}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_090}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_18RS21}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_2603}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_COH1}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_M732}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_M781}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
Consensus	*****	*****	*****	*_...*****	*****
msa141507.2{399_A909}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_CJB110}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_H36B}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_JM9130013}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_1169NT}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_090}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_18RS21}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_2603}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_COH1}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_M732}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_M781}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
Consensus	**_*****	*****	*****	*****	*****
msa141507.2{399_A909}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_CJB110}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_H36B}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_JM9130013}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_1169NT}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_090}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_18RS21}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_2603}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_COH1}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_M732}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_M781}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_CJB110}	AACCCCTAAA	ACAAATGTTA	GG-----	--	
msa141507.2{399_H36B}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_JM9130013}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_1169NT}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_090}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_18RS21}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_2603}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_COH1}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_M732}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_M781}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
Consensus	*****	*****	*****	---	

SEQ ID NO. 7812

STRAIN 2603 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPLLIIFATAYDQYAIQAFEHDDARDYLLKPYDFDRLKQAMDRVKALST

Table 78: Comparative Sequences relating to SAG1016

STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7813

STRAIN 090 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7814

STRAIN A909 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7815

STRAIN H36B frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7816

STRAIN 18RS21 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7817

STRAIN M732 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVAGSGLPKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7818

STRAIN COH1 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVAGSGLPKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7819

STRAIN M781 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVAGSGLPKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7820

STRAIN CJB110 frame: 1

LNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG LQLAEYINKMPKPPLLI F
ATAYDQYAI QAFEHDARDYLLKPYEFDRLKQXMDRVKGALSTSTIIESVTSGPLFKQQYPL
TVEDXIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQWQDKLPSSQFVRVHRSYI
VNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQML

SEQ ID NO. 7821

STRAIN 1169NT frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDIATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7822

STRAIN JM9130013 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

Table 78: Comparative Sequences relating to SAG1016

PRETTY of: /biotmp/msa141801.2{*} April 10, 2003 06:38 ..

	1				50
msa141801.2{399_COH1}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_M732}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_M781}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_090}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_18RS21}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_2603}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_A909}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_H36B}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_JM9130013}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_1169NT}	kvlvvdddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_CJB110}	-----LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL	
Consensus	-----	*****	*****	***-*****	*****
	51				100
msa141801.2{399_COH1}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EqDARDYLLK
msa141801.2{399_M732}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EqDARDYLLK
msa141801.2{399_M781}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EqDARDYLLK
msa141801.2{399_090}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_18RS21}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_2603}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_A909}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_H36B}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_JM9130013}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_1169NT}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_CJB110}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
Consensus	*****	*****	*****	*****	*-*****
	101				150
msa141801.2{399_COH1}	PYeFDRLKQa	MDRVKGALST	STIIESVaSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_M732}	PYeFDRLKQa	MDRVKGALST	STIIESVaSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_M781}	PYeFDRLKQa	MDRVKGALST	STIIESVaSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_090}	PYdFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_18RS21}	PYdFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_2603}	PYdFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_A909}	PYeFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_H36B}	PYeFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_JM9130013}	PYeFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_1169NT}	PYeFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_CJB110}	PYeFDRLKQx	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDxIYLVSA
Consensus	**--*****-	*****	*****	*****	***-*****
	151				200
msa141801.2{399_COH1}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_M732}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_M781}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_090}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_18RS21}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_2603}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_A909}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_H36B}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_JM9130013}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_1169NT}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_CJB110}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
Consensus	*****	*****	*****	*****	*****
	201				243
msa141801.2{399_COH1}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_M732}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_M781}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_090}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_18RS21}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_2603}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_A909}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_H36B}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_JM9130013}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_1169NT}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_CJB110}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQML-	---
Consensus	*****	*****	*****	*****	---

Table 79: Comparative Sequences relating to SAG2150

SEQ ID NO. 7901

STRAIN 2603

ATGGGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCCGGCACTCCCTTTTGAAGGG
 CGTGCCCTTTTGGAGCTCAATCTGAAAATGAAGATGCTTCTATACCGCGTTTCATTGGG
 CACACAGGTTCTGGAAAATCACTATTATGCAACTTTTGAATGGTTTACATATTCTTACA
 AAAGGTGAGGTAATTTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATC
 AAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTCAGCTTTTGA
 GAGACAGTTTAAAGGATGTTGCTTTGGACCACAAAATTTTGGTATTTCTCAGATTGAA
 GCTGAAAGGCTGGCTGAAGAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTTCGAT
 AAAAAATCCATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTGTCTATAGCTGGTATTTTA
 GCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGA
 AGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTATCGTCTTA
 GTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTATGTGTATGTTTGAAGCA
 GGGAAAGTAACCTTATCAGGACAACCAAAACAGATTTTCAAGAAGTAGAATTTTAGAA
 AGTAAACAATTAGGAGTTCCCAAAATCACCAGTTTGCTCAAAGACTATCTCATAAGGGA
 TTAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7902

STRAIN 090

GGAAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
 GGCACCTCCCTTTTGAAGGGCGTGCCCTTTTGGAGCTCAATCTGAAAATTTGA
 AGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCTGGAAAATCAA
 CTATTATGCAACTTTTGAATGGTTTACATATTCTTACAAAAGGTGAGGTA
 ATTGTGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
 ATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTCAGC
 TTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
 GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAATTAAGGTT
 AGTTGGTATCAGTGAGGATTTATTTCGATAAAAATCCATTGAACTTTCTG
 GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
 AAGTACTAGTACTGGATGAGCCACAGCTGGACTTGATCCTAAGGGAAG
 AAAAGAATTAAAGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTA
 TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
 GTGTATGTTTGAAGCAGGGGAAAGTAACCTTATCAGGACAACCAAAACA
 GATTTTCAAGAAGTAGAATTTTGAAGTAACAATAGGAGTTCCCA
 AATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
 AGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7903

STRAIN A909

GGAAATTGAATTTAAAAATGTAAGTTATACCTATCAA
 GCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGAGCTCAATCTGAAAAT
 TGAAGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCTGGAAAAT
 CACTATTATGCAACTTTTGAATGGTTTACATATTCTTACAAAAGGTGAG
 GTAATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAAT
 CAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTC
 AGCTTTTGAAGAGACAGTTTAAAGATGTTGCTTTTGGACCACAAAAT
 TTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAATTAAG
 GTTAGTTGGTATCAGTGAGGATTTATTTCGATAAAAATCCATTGAACTTT
 CTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGA
 CCCAAAGTACTAGTACTAGATGAGCCACAGCTGGACTTGATCCTAAGGG
 AAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGA
 CTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGAC
 TATGTGTATGTTTGAAGCAGGGGAAAGTAACCTTATCAGGACAACCAAA
 GCAGATTTTCAAGAAGTAGAATTTTGAAGTAACAATAGGAGTTTCC
 CCAAAATCACCAGTTTGTCTCAAAGGCTATCTCATAAGGGATTAAATTTA
 CCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGG
 A

SEQ ID NO. 7904

STRAIN H36B

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGAGCTCAATC
 TGAATAATTGAAGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCT
 GGAAAATCACTATTATGCAACTTTTGAATGGTTTACATATTCTTACAAA
 AGGTGAGGTAATTTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGGTTAGTTGGTATCAGTGAGGATTTATTTCGATAAAAATCCATT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTAGATGAGCCACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGGAAAGTAACCTTATCAGGAC
 AACCAAGCAGATTTTCAAGAAGTAGAATTTTGAAGTAACAATTA
 GGAGTTCCCAAAATCACCAGTTTGTCTCAAAGGCTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7905

STRAIN 18RS21

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGAGCTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
 AGGTGAGGTAATGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGTTAGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATT
 GAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7906

STRAIN M732

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGCGTGCCCTTTTGGACGTCAATC
 TGAAAATTGAAGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
 AGGTGAGGTAATGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGTTAGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATT
 GAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7907

STRAIN COH1

GGAAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
 GGCATCCTCTTTGAAGGCGTGCCCTTTTGGACGTCAATCTGAAAATTGA
 AGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAATCAA
 CTATTATGCAACTTTTGAATGGTTTACATATTCTACAAAAGGTGAGGTA
 ATTGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
 ATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTCAGC
 TTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTT
 GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAATTAAGGTT
 AGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATTGAACTTTCTG
 GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
 AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGAAG
 AAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAAGGAATGACTA
 TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
 GTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAAACA
 GATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTAGGAGTTCCCA
 AAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
 AGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7908

STRAIN M781

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGCGTGCCCTTTTGGACGTCAATC
 TGAAAATTGAAGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
 AGGTGAGGTAATGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGTTAGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATT
 GAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7909

STRAIN CJB110

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGCGTGCCCTTTTGGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCT
 GGGAAATCAACTATTATGCACTTTTGAATGGTTTACATATTCCTACAAA
 AGGTGAGGTAATGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAAC
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTCAATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATT
 GAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCCTGACTATGTGTATGTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAAACAATTA
 GGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7910

STRAIN 1169NT

GGAATTGAATTTAAAAATGTAA

GTATACCTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGAC
 GTCAATCTGAAAATTGAAGATGCTTCTATACCGCGTTTCATTGGGCACAC
 AGGTTCTGGAATAATCAACTATTATGCAACTTTTGAATGGTTTACATATTC
 CTACAAAAGGTGAGGTAATTTGTGCGATGATTTTCTATTAAAGCAGGGGAC
 AAGAACAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTTCA
 ATTTCCAGAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTT
 TTGGACACACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCT
 GAAGAAAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAA
 TCCATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTA
 TTTTAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGA
 CTTGATCTTAAGGGAAGAAAAGAAATTAATGACTCTTTTAAAAATCTTCA
 TAAAAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAG
 CGGATTATGCTGACTATGTGTATGTTTAGAAGCAGGGAAAGTAACCTTA
 TCAGGACAACCAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAA
 ACAATTAGGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATA
 AGGGATTAAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAG
 GCTATTAAGCATGGA

SEQ ID NO. 7911

STRAIN JM9130013

GGAATTGAATTTAAAAATGTAAAGTT

ATACCTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTT
 AATCTGAAAATTGAAGATGCTTCTATACCGCATTTCATTGGGCACACAGG
 TTCTGGAATAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTA
 CAAAAGGTGAGGTAATTTGTGCGATGATTTTCTATTAAAGCAGGGGACAAG
 AACAAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTTCAAT
 TCCAGAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTG
 GACCACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAA
 GAAAAATTAAGGTTAGTTGGTATTAGTGAGGATTTATTCGATAAAAATCC
 ATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTT
 TAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTT
 GATCTTAAGGGAAGAAAAGAAATTAATGACTCTTTTAAAAATCTTCATAA
 AAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGG
 ATTATGCTGACTATGTGTATGTTTAGAAGCAGGGAAAGTAACCTTATCA
 GGACAACCAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAAACA
 ATTAGGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGG
 GATTAAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCT
 ATTAAGCATGGA

PRETTY of: /biotmp/msa238454.2{*} May 14, 2003 06:55 ..

	1		50
msa238454.2{401_A909}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_H36B}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_090}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_1169NT}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_18RS21}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_2603}	atgGGAATTG	AATTTAAAAA	TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_CJB110}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_COH1}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_M732}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_M781}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_JM9130013}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT ACCTATCAAG CCGGCACTCC
Consensus	*****	*****	*****
	51		100
msa238454.2{401_A909}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA TCTGAAAATT GAAGATGcTT
msa238454.2{401_H36B}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA TCTGAAAATT GAAGATGcTT
msa238454.2{401_090}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA TCTGAAAATT GAAGATGcTT
msa238454.2{401_1169NT}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA TCTGAAAATT GAAGATGcTT
msa238454.2{401_18RS21}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA TCTGAAAATT GAAGATGcTT
msa238454.2{401_2603}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA TCTGAAAATT GAAGATGcTT
msa238454.2{401_CJB110}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA TCTGAAAATT GAAGATGcTT

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_COH1}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAAAT	GAAGATGtTT
msa238454.2{401_M732}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAAAT	GAAGATGtTT
msa238454.2{401_M781}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAAAT	GAAGATGtTT
msa238454.2{401_JM9130013}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAAAT	GAAGATGcTT
Consensus	*****	*****	*****_*	*****	*****_*
msa238454.2{401_A909}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_H36B}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_090}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_1169NT}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_18RS21}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_2603}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_CJB110}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_COH1}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_M732}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_M781}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
msa238454.2{401_JM9130013}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAAATC	AACTATTATG
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_H36B}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_090}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_1169NT}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_18RS21}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_2603}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_CJB110}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_COH1}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_M732}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_M781}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_JM9130013}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_H36B}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_090}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_1169NT}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_18RS21}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_2603}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_CJB110}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_COH1}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_M732}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_M781}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_JM9130013}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_H36B}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_090}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_1169NT}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_18RS21}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_2603}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_CJB110}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_COH1}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_M732}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_M781}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_JM9130013}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_H36B}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_090}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_1169NT}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_18RS21}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_2603}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_CJB110}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_COH1}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_M732}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_M781}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_JM9130013}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_H36B}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_090}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_1169NT}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_18RS21}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_2603}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_CJB110}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_COH1}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_M732}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_M781}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_JM9130013}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_H36B}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_090}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_1169NT}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_18RS21}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_2603}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_CJB110}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_COH1}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_M732}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_M781}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_JM9130013}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
Consensus	*-*****	*****	*****	*****	*****
msa238454.2{401_A909}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_H36B}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_090}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_1169NT}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_18RS21}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_2603}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_CJB110}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_COH1}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_M732}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_M781}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_JM9130013}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	AGTACTaGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_H36B}	AGTACTaGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_090}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_1169NT}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_18RS21}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_2603}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_CJB110}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_COH1}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_M732}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_M781}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_JM9130013}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
Consensus	*****-***	*****	*****	*****	*****
msa238454.2{401_A909}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_H36B}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_090}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_1169NT}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_18RS21}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_2603}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_CJB110}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_COH1}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_M732}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_M781}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_JM9130013}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_H36B}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_090}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_1169NT}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_18RS21}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_2603}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_CJB110}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_COH1}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_M732}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_M781}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_JM9130013}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAag	CAGATTTTTTC
msa238454.2{401_H36B}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAag	CAGATTTTTTC
msa238454.2{401_090}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTTC
msa238454.2{401_1169NT}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTTC
msa238454.2{401_18RS21}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTTC

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_2603}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_CJB110}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_COH1}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_M732}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_M781}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_JM9130013}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
Consensus	*****	*****	*****	*****	*****
701					
msa238454.2{401_A909}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_H36B}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_090}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_1169NT}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_18RS21}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_2603}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_CJB110}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_COH1}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_M732}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_M781}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_JM9130013}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
Consensus	*****	*****	*****	*****	*****
751					
msa238454.2{401_A909}	AAGTTTGCTC	AAAGgCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_H36B}	AAGTTTGCTC	AAAGgCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_090}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_1169NT}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_18RS21}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_2603}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_CJB110}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_COH1}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_M732}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_M781}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_JM9130013}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
Consensus	*****	*****	*****	*****	*****
801					
msa238454.2{401_A909}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_H36B}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_090}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_1169NT}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_18RS21}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_2603}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_CJB110}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_COH1}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_M732}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_M781}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_JM9130013}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
Consensus	*****	*****	*****	*****	
840					
SEQ ID NO. 7912					
STRAIN 2603 frame: 1					
MGIEFKNVSYTYQAGTTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK					
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA					
ERLAEEKLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR					
KELMTLFLKNLHKKGMTIVLVTHLMDVDVADYADYVYVLEAGKVTLSGQPKQIFQEVVELLES					
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG					
SEQ ID NO. 7913					
STRAIN 090 frame: 1					
GIEFKNVSYTYQAGTTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK					
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA					
ERLAEEKLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR					
KELMTLFLKNLHKKGMTIVLVTHLMDVDVADYADYVYVLEAGKVTLSGQPKQIFQEVVELLES					
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG					
SEQ ID NO. 7914					
STRAIN 090 frame: 1					
GIEFKNVSYTYQAGTTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK					
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA					
ERLAEEKLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR					
KELMTLFLKNLHKKGMTIVLVTHLMDVDVADYADYVYVLEAGKVTLSGQPKQIFQEVVELLES					
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG					
SEQ ID NO. 7915					
STRAIN H36B frame: 1					
GIEFKNVSYTYQAGTTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK					
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA					
ERLAEEKLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR					
KELMTLFLKNLHKKGMTIVLVTHLMDVDVADYADYVYVLEAGKVTLSGQPKQIFQEVVELLES					
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG					
SEQ ID NO. 7916					

Table 79: Comparative Sequences relating to SAG2150

STRAIN 18RS21 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSGKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7917

STRAIN M732 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTSGSGKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7918

STRAIN COH1 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTSGSGKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7919

STRAIN M781 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTSGSGKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7920

STRAIN CJB110 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSGKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7921

STRAIN 1169NT frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSGKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7922

STRAIN JM9130013 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSGKSTIMQLLNLGHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

PRETTY of: /biotmp/msa238553.2{*} May 14, 2003 06:55 ..

	1		50
msa238553.2{401_090}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_1169NT}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_18RS21}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_2603}	mGIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_CJB110}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_H36B}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_JM9130013}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_COH1}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDvSYTAFIG HTGSGKSTIM	
msa238553.2{401_M732}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDvSYTAFIG HTGSGKSTIM	
msa238553.2{401_M781}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDvSYTAFIG HTGSGKSTIM	
Consensus	*****	*****	**-*****
	51		100
msa238553.2{401_090}	QLLNLGHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_1169NT}	QLLNLGHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_18RS21}	QLLNLGHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_2603}	QLLNLGHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_CJB110}	QLLNLGHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_H36B}	QLLNLGHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_JM9130013}	QLLNLGHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_COH1}	QLLNLGHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_M732}	QLLNLGHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_M781}	QLLNLGHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	

Table 79: Comparative Sequences relating to SAG2150

Consensus	*****	*****	*****	*****	*****
	101				150
msa238553.2{401_090}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_1169NT}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_18RS21}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_2603}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_CJB110}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_H36B}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_JM9130013}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_COH1}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_M732}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_M781}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
Consensus	*****	*****	*****	*****	*****
	151				200
msa238553.2{401_090}	MRRVAIAGIL	AMEPKVLVD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_1169NT}	MRRVAIAGIL	AMEPKVLVD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_18RS21}	MRRVAIAGIL	AMEPKVLVD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_2603}	MRRVAIAGIL	AMEPKVLVD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_CJB110}	MRRVAIAGIL	AMEPKVLVD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_H36B}	MRRVAIAGIL	AMEPKVLVD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_JM9130013}	MRRVAIAGIL	AMEPKVLVD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_COH1}	MRRVAIAGIL	AMEPKVLVD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_M732}	MRRVAIAGIL	AMEPKVLVD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_M781}	MRRVAIAGIL	AMEPKVLVD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
Consensus	*****	*****	*****	*****	*****
	201				250
msa238553.2{401_090}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_1169NT}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_18RS21}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_2603}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_CJB110}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_H36B}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_JM9130013}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_COH1}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_M732}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_M781}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
Consensus	*****	*****	*****	*****	*****
	251				280
msa238553.2{401_090}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_1169NT}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_18RS21}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_2603}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_CJB110}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_H36B}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_JM9130013}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_COH1}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_M732}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_M781}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
Consensus	*****	*****	*****		

Table 80: Comparative Sequences relating to SAG1266

SEQ ID NO. 8001

STRAIN 2603

GTGAACCACTTACTTAACCTCAGTAAAGAAAATATAGCTAAAATAGATTTTGACTTTCTT
 AATGAGGCACCTTAATGCAAAATATTCGTTTGAAAGAATTAGTAGATGAACATAAAATTTCA
 AAAGAACTGGACAGTAAAGGTTGGTCCAAAAAGACTCTCGAACGATAAAAAATCTTGATAC
 GATGGCCTTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCAA
 GTCATTCCATTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAAGGAGAAATCT
 AAAAATTATAGAAATACAACTACAGTGATTATGAAATGGAGTTAATCAATGAGGATAGG
 CAACAATTTTCAAAATATGAAACAGTTGATTTAGACCAATTGATACTTGTGTATATTTT
 AATATTGATGACTACATTTTCATCATATTTAACAATA

SEQ ID NO. 8002

STRAIN H36B

AACCACTTACTTAACCTCAGTAAAGAAAATATAGCT
 AAAATAGATTTTGACTTTCTTAATGAGGCACCTTAATGCAAAATATTCGTTT
 GAAAGAATTAGTAGATGAACATAAAATTTCAAAGAAGCTGGACAGTAAAG
 GTTGGTCCAAAAAGACTCTCGAACGATAAAAAATCTTGACGATGGCCTT
 ATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCA
 AGTCATTCCATTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAA
 GGGAGAATTCTAAAAATATAGAAATATACAACTACAGTGATTATGAAATG
 GAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTTGA
 TTTAGACCAATTGATACTTGTGTATATTTTAATATTGATGACTACATT
 CATCATATTTAACAATA

SEQ ID NO. 8003

STRAIN 18RS21

AACCACTTACTTAACCTCAGTAAAGAAAATATAG
 CTAAAAATAGATTTTGACTTTCTTAATGAGGCACCTTAATGCAAAATATTCGTT
 TTGAAAGAAATTAGTAGATGAACATAAAATTTCAAAGAAGCTGGACAGTAA
 AGGTTGGTCCAAAAAGACTCTCGAACGATAAAAAATCTTGACGATGGCCTT
 TTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATC
 CAAGTCATTCCATTGCTAATGTACATGTACTACTGTTTTTAATACCAGA
 AAGGGAGAAATCTAAAAATATAGAAATATACAACTACAGTGATTATGAAA
 TGGAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTT
 GATTTAGACCAATTGATACTTGTGTATATTTTAATATTGATGACTACAT
 TTCATCATATTTAACAATA

PRETTY of: /biotmp/msa49308.2{*} February 19, 2003 07:45 ..

	1		50
msa49308.2{408_18RS21}	---AACCACCT	TACTTAACCT	CAGTAAAGAA AATATAGCTA AAATAGATT
msa49308.2{408_2603}	gtgAACCACCT	TACTTAACCT	CAGTAAAGAA AATATAGCTA AAATAGATT
msa49308.2{408_H36B}	---AACCACCT	TACTTAACCT	CAGTAAAGAA AATATAGCTA AAATAGATT
Consensus	*****	*****	*****
	51		100
msa49308.2{408_18RS21}	TGACTTTCTT	AATGAGGCAC	TTAATGCAAA TATTCGTTTG AAAGAATTAG
msa49308.2{408_2603}	TGACTTTCTT	AATGAGGCAC	TTAATGCAAA TATTCGTTTG AAAGAATTAG
msa49308.2{408_H36B}	TGACTTTCTT	AATGAGGCAC	TTAATGCAAA TATTCGTTTG AAAGAATTAG
Consensus	*****	*****	*****
	101		150
msa49308.2{408_18RS21}	TAGATGAACCT	AAAAATTTCA	AAAGAACTGG ACAGTAAAGG TTGGTCCAAA
msa49308.2{408_2603}	TAGATGAACCT	AAAAATTTCA	AAAGAACTGG ACAGTAAAGG TTGGTCCAAA
msa49308.2{408_H36B}	TAGATGAACCT	AAAAATTTCA	AAAGAACTGG ACAGTAAAGG TTGGTCCAAA
Consensus	*****	*****	*****
	151		200
msa49308.2{408_18RS21}	AAAGACTCTC	GAACGATAAA	AATCTTGTAC GATGGCCTTA TCAATAAACA
msa49308.2{408_2603}	AAAGACTCTC	GAACGATAAA	AATCTTGTAC GATGGCCTTA TCAATAAACA
msa49308.2{408_H36B}	AAAGACTCTC	GAACGATAAA	AATCTTGTAC GATGGCCTTA TCAATAAACA
Consensus	*****	*****	*****
	201		250
msa49308.2{408_18RS21}	TATAGTTTCC	CTAGATCGTG	CAGATTATAA CATTATCCAA GTCATTCCAT
msa49308.2{408_2603}	TATAGTTTCC	CTAGATCGTG	CAGATTATAA CATTATCCAA GTCATTCCAT
msa49308.2{408_H36B}	TATAGTTTCC	CTAGATCGTG	CAGATTATAA CATTATCCAA GTCATTCCAT
Consensus	*****	*****	*****
	251		300
msa49308.2{408_18RS21}	TTGCTAATGT	ACATGTACTA	CTGTTTTTAA TACCAGAAAG GGAGAATTCT
msa49308.2{408_2603}	TTGCTAATGT	ACATGTACTA	CTGTTTTTAA TACCAGAAAG GGAGAATTCT
msa49308.2{408_H36B}	TTGCTAATGT	ACATGTACTA	CTGTTTTTAA TACCAGAAAG GGAGAATTCT
Consensus	*****	*****	*****
	301		350
msa49308.2{408_18RS21}	AAAAATTATA	GAATATACAA	CTACAGTGAT TATGAAATGG AGTTAATCAA
msa49308.2{408_2603}	AAAAATTATA	GAATATACAA	CTACAGTGAT TATGAAATGG AGTTAATCAA
msa49308.2{408_H36B}	AAAAATTATA	GAATATACAA	CTACAGTGAT TATGAAATGG AGTTAATCAA
Consensus	*****	*****	*****

Table 80: Comparative Sequences relating to SAG1266

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351                                     400
msa49308.2{408_18RS21} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
msa49308.2{408_2603} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
msa49308.2{408_H36B} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
Consensus *****

401                                     450
msa49308.2{408_18RS21} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
msa49308.2{408_2603} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
msa49308.2{408_H36B} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
Consensus *****

451
msa49308.2{408_18RS21} ACAATA
msa49308.2{408_2603} ACAATA
msa49308.2{408_H36B} ACAATA
Consensus *****

SEQ ID NO. 8004
STRAIN 2603 frame: 1
VNHLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILY
DGLINKHIVSLDRADYNI IQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDR
QQFSKYETVDLDQLILVDIFNIDDISSYLTII

SEQ ID NO. 8005
STRAIN H36B frame: 1
NHLLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNI IQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDRQ
QFSKYETVDLDQLILVDIFNIDDISSYLTII

SEQ ID NO. 8006
STRAIN 18RS21 frame: 1
NHLLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNI IQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDRQ
QFSKYETVDLDQLILVDIFNIDDISSYLTII

PRETTY of: /biotmp/msa49418.2{*} February 19, 2003 07:47 ..

1                                     50
msa49418.2{408_18RS21} -NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
msa49418.2{408_2603} vNHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
msa49418.2{408_H36B} -NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
Consensus *****

51                                     100
msa49418.2{408_18RS21} KDSRTIKILY DGLINKHIVS LDRADYNI IQ VIPFANVHVL LFLIPERENS
msa49418.2{408_2603} KDSRTIKILY DGLINKHIVS LDRADYNI IQ VIPFANVHVL LFLIPERENS
msa49418.2{408_H36B} KDSRTIKILY DGLINKHIVS LDRADYNI IQ VIPFANVHVL LFLIPERENS
Consensus *****

101                                    150
msa49418.2{408_18RS21} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
msa49418.2{408_2603} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
msa49418.2{408_H36B} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
Consensus *****

151
msa49418.2{408_18RS21} TI
msa49418.2{408_2603} TI
msa49418.2{408_H36B} TI
Consensus **

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Table 81: Comparative Sequences relating to SAG0011

SEQ ID NO. 8101

STRAIN 090

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTT
 ACAAGAACGTCGTCAGAAGTTGTAAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTGCTAGCAAAACAATAAAAAAT
 CCAGATTACGTTCAAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGCGAAATGATTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8102

STRAIN A909

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATA
 TATTAAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCG
 TTTAATGGGTTGGGTTCTTATTTTGTCTATGCTtttATTTATTTTACCCACTTATAATTT
 AGTTAAGAGTTACAGAACCTTTACAAGAACGTCGTCAGAAGTTGTAAAAATTAACGAAAGA
 CTATCAGACATTAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAA
 TCCAGATTACGTTCAAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGCGAAAT
 GATTTACCCATTACCAGACCT

SEQ ID NO. 8103

STRAIN H36B

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTT
 ACAAGAACGTCGTCAGAAGTTGTAAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAAT
 CCAGATTACGTTCAAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGCGAAATGATTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8104

STRAIN 18RS21

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATATATTAACGATGAGAATCTAAAAA
 CGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTT
 GTCATGCTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTACAA
 GAACGTCGTCAGAAGTTGTAAAAATTAACGAAAGACTATCAGACATTAACTAATAGAACT
 GAGAACCAGAAGTTGCTAGCAAAACAATAAAAAATCCAGATTACGTTCAAAAAATATGCT
 CGAGCTAAGTATTATTTCTCTAAGACCGCGAAATGATTTACCCATTACCAGACCTTTTA
 CCAAAA

SEQ ID NO. 8105

STRAIN M732

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTT
 ACAAGAACGTCGTCAGAAGTTGTAAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAAT
 CCAGATTACGTTCAAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGAC
 CGCGAAATGATTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8106

STRAIN COH1

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATGCTttt
 ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTTACAAG
 AACGTCGTCAGAAGTTGTAAAAATTAACGAAAGACTATCAGACATTAACT
 AATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAATCCAGA
 TTACGTTCAAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGACCGGCG
 AATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8107

STRAIN M781

AGCaAGCCTAATGTTGTTTCAGTT
 AAATAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTG
 AGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATGCT
 ATGCTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAAC
 TTTACAAGAACGTCGTCAGAAGTTGTAAAAATTAACGAAAGACTATCAGA
 CATTAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAA
 AATCCAGATTACGTTCAAAAAATATGCTCGAGCGAAGTATTATTTCTCTA
 GACCGCGAAATGATTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8108

STRAIN CJB110

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATGCTttt
 ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTTACAAG

Table 81: Comparative Sequences relating to SAG0011

AACGTCGTCAGAAGTTGTAAATTAACGAAAGACTATCAGACATTAAC
 AATAGAAGTGAAGACCAGAAGTTGCTAGCAAAACAACTAAAAATCCAGA
 TTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGGCG
 AAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8109

STRAIN 1169NT

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTT
 ACAAGAAGCTCGTCAAGAAGTTGTAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAAGTGAAGACCAGAAGTTACTAGCAAAACAACTAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGCGAAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8110

STRAIN JM9130013

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTT
 ACAAGAAGCTCGTCAAGAAGTTGTAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAAGTGAAGACCAGAAGTTACTAGCAAAACAACTAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 TGGCGAAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8111

STRAIN 2603

agcaagcctaagtgtgttcagttaataatcaatatattaacgatgagaa
 tctaaaaaacgttacgaagctgaggagttacgccgaaaaaatcgtttaa
 tgggttgggttcttattttgtcatgcttttatttttaccacttat
 aatttagttaagagttacagaactttacaagaacgtcgtcaagaagttgt
 aaaattaacgaagactatcagacattaactaatagaactgagaaccaga
 agttgctagcaaaacaactaaaaatccagattacgttcaaaaatgatgct
 cgagctaagttattttctctaagaccggcgaaatgatttaccattacc
 agaccttttaccaaaa

PRETTY of: /biotmp/msa25643.2{*} . April 29, 2002 05:59 ..

	1		50
msa25643.2{418_COH1}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_M732}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_M781}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_JM9130013}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_090}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_18RS21}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_2603}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_CJB110}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_1169NT}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_A909}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_H36B}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
Consensus	*****	*****	*****
	51		100
msa25643.2{418_COH1}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_M732}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_M781}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_JM9130013}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_090}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_18RS21}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_2603}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_CJB110}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_1169NT}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_A909}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_H36B}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
Consensus	*****	*****	*****
	101		150
msa25643.2{418_COH1}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_M732}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_M781}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_JM9130013}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_090}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_18RS21}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_2603}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_CJB110}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_1169NT}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_A909}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_H36B}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
Consensus	*****	*****	*****

Table 81: Comparative Sequences relating to SAG0011

	151		200
msa25643.2{418_COH1}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA GAACGTCGTC AAGAAGTTGT
msa25643.2{418_M732}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA GAACGTCGTC AAGAAGTTGT
msa25643.2{418_M781}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA GAACGTCGTC AAGAAGTTGT
msa25643.2{418_JM9130013}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA GAACGTCGTC AAGAAGTTGT
msa25643.2{418_090}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA GAACGTCGTC AAGAAGTTGT
msa25643.2{418_18RS21}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA GAACGTCGTC AAGAAGTTGT
msa25643.2{418_2603}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA GAACGTCGTC AAGAAGTTGT
msa25643.2{418_CJB110}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA GAACGTCGTC AAGAAGTTGT
msa25643.2{418_1169NT}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA GAACGTCGTC AAGAAGTTGT
msa25643.2{418_A909}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA GAACGTCGTC AAGAAGTTGT
msa25643.2{418_H36B}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA GAACGTCGTC AAGAAGTTGT
Consensus	*****	*****	*****
	201		250
msa25643.2{418_COH1}	AAAATTAACG	AAAGACTATC	AGACATTAAC TAATAGAACT GAGAACCAGA
msa25643.2{418_M732}	AAAATTAACG	AAAGACTATC	AGACATTAAC TAATAGAACT GAGAACCAGA
msa25643.2{418_M781}	AAAATTAACG	AAAGACTATC	AGACATTAAC TAATAGAACT GAGAACCAGA
msa25643.2{418_JM9130013}	AAAATTAACG	AAAGACTATC	AGACATTAAC TAATAGAACT GAGAACCAGA
msa25643.2{418_090}	AAAATTAACG	AAAGACTATC	AGACATTAAC TAATAGAACT GAGAACCAGA
msa25643.2{418_18RS21}	AAAATTAACG	AAAGACTATC	AGACATTAAC TAATAGAACT GAGAACCAGA
msa25643.2{418_2603}	AAAATTAACG	AAAGACTATC	AGACATTAAC TAATAGAACT GAGAACCAGA
msa25643.2{418_CJB110}	AAAATTAACG	AAAGACTATC	AGACATTAAC TAATAGAACT GAGAACCAGA
msa25643.2{418_1169NT}	AAAATTAACG	AAAGACTATC	AGACATTAAC TAATAGAACT GAGAACCAGA
msa25643.2{418_A909}	AAAATTAACG	AAAGACTATC	AGACATTAAC TAATAGAACT GAGAACCAGA
msa25643.2{418_H36B}	AAAATTAACG	AAAGACTATC	AGACATTAAC TAATAGAACT GAGAACCAGA
Consensus	*****	*****	*****
	251		300
msa25643.2{418_COH1}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG ATTACGTTCA AAAATATGCT
msa25643.2{418_M732}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG ATTACGTTCA AAAATATGCT
msa25643.2{418_M781}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG ATTACGTTCA AAAATATGCT
msa25643.2{418_JM9130013}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG ATTACGTTCA AAAATATGCT
msa25643.2{418_090}	AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG ATTACGTTCA AAAATATGCT
msa25643.2{418_18RS21}	AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG ATTACGTTCA AAAATATGCT
msa25643.2{418_2603}	AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG ATTACGTTCA AAAATATGCT
msa25643.2{418_CJB110}	AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG ATTACGTTCA AAAATATGCT
msa25643.2{418_1169NT}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG ATTACGTTCA AAAATATGCT
msa25643.2{418_A909}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG ATTACGTTCA AAAATATGCT
msa25643.2{418_H36B}	AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG ATTACGTTCA AAAATATGCT
Consensus	****-****	*****	*****
	301		350
msa25643.2{418_COH1}	CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC GAAATGATTT ACCCATTACC
msa25643.2{418_M732}	CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC GAAATGATTT ACCCATTACC
msa25643.2{418_M781}	CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC GAAATGATTT ACCCATTACC
msa25643.2{418_JM9130013}	CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC GAAATGATTT ACCCATTACC
msa25643.2{418_090}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC GAAATGATTT ACCCATTACC
msa25643.2{418_18RS21}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC GAAATGATTT ACCCATTACC
msa25643.2{418_2603}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC GAAATGATTT ACCCATTACC
msa25643.2{418_CJB110}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC GAAATGATTT ACCCATTACC
msa25643.2{418_1169NT}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC GAAATGATTT ACCCATTACC
msa25643.2{418_A909}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC GAAATGATTT ACCCATTACC
msa25643.2{418_H36B}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC GAAATGATTT ACCCATTACC
Consensus	*****	*****	*****
	351		366
msa25643.2{418_COH1}	AGACCTttta	ccaaaa	
msa25643.2{418_M732}	AGACCTttta	ccaaaa	
msa25643.2{418_M781}	AGACCTttta	ccaaaa	
msa25643.2{418_JM9130013}	AGACCTttta	ccaaaa	
msa25643.2{418_090}	AGACCTttta	ccaaaa	
msa25643.2{418_18RS21}	AGACCTttta	ccaaaa	
msa25643.2{418_2603}	AGACCTttta	ccaaaa	
msa25643.2{418_CJB110}	AGACCTttta	ccaaaa	
msa25643.2{418_1169NT}	AGACCTttta	ccaaaa	
msa25643.2{418_A909}	AGACCT~~~~	~~~~~	
msa25643.2{418_H36B}	AGACCTttta	ccaaaa	
Consensus	*****	-----	

SEQ ID NO. 8112

STRAIN 090

SKPNVQVLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
VKSRYTLQERRQEVVKLTQDYQTLTNRTNENQKLLAKQLKNPDYVQKYARAKYFSKTGEM
IYPLDLLPK

SEQ ID NO. 8113

STRAIN A909

SKPNVQVLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
VKSRYTLQERRQEVVKLTQDYQTLTNRTNENQKLLAKQLKNPDYVQKYARAKYFSKTGEM

Table 81: Comparative Sequences relating to SAG0011

IYPLPD

SEQ ID NO. 8114

STRAIN H36B

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYF SKTGEM
 IYPLPDLLPK

SEQ ID NO. 8115

STRAIN 18RS21

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL VKSYRTLQ
 ERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYF SKTGEM IYPLPDLL
 PK

SEQ ID NO. 8116

STRAIN M732

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYF SKTGEM
 IYPLPDLLPK

SEQ ID NO. 8117

STRAIN COH1

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVK
 SYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYF SKTGEM IY
 PLPDLLPK

SEQ ID NO. 8118

STRAIN M781

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 LVKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYF SKTGE
 MIYPLPDLLPK

SEQ ID NO. 8119

STRAIN CJB110

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVK
 SYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYF SKTGEM IY
 PLPDLLPK

SEQ ID NO. 8120

STRAIN 1169NT

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYF SKTGEM
 IYPLPDLLPK

SEQ ID NO. 8121

STRAIN JM9130013

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYF SKTGEM
 IYPLPDLLPK

SEQ ID NO. 8122

STRAIN 2603

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL VKSYRTLQ
 ERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYF SKTGEM IYPLPDLL
 PK

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa20122.2{*} April 29, 2002 06:08 ..

	1		50
msa20122.2{418_090}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_A909}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_1169NT}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_18RS21}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_2603}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_CJB110}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_COH1}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_H36B}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_JM9130013}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_M732}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
msa20122.2{418_M781}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK	NRLMGWVLIF VMLLFILPTY
Consensus	*****	*****	*****
	51		100
msa20122.2{418_090}	NLVKSRYRTLQ	ERRQEVVVKLT KDYQTLTNRT	ENQKLLAKQL KNPDYVQKYA
msa20122.2{418_A909}	NLVKSRYRTLQ	ERRQEVVVKLT KDYQTLTNRT	ENQKLLAKQL KNPDYVQKYA

Table 81: Comparative Sequences relating to SAG0011

msa20122.2{418_1169NT}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_18RS21}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_2603}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_CJB110}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_COH1}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_H36B}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_JM9130013}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_M732}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_M781}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
Consensus	*****	*****	*****	*****	*****

	101	122
msa20122.2{418_090}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_A909}	RAKYFSGKTG	EMIYPLPD-- --
msa20122.2{418_1169NT}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_18RS21}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_2603}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_CJB110}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_COH1}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_H36B}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_JM9130013}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_M732}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_M781}	RAKYFSGKTG	EMIYPLPD11 pk
Consensus	*****	*****-- --

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8201

STRAIN 2603

ATGAAAAATTATTGTTAAAAATGTAAGGATAAGAAGGTTAAAGCATTTACACTTTTAGAA
 TGTGTTGGTAGCATTGGTTACAATCACAGGAGCTTTACTAGTTTATCAAGGACTGACAAAA
 TTGTTGGCTCAACAGATAGTAGTGATGCTTCTCCAGTCAGTCTGAATGGGTGTTATTA
 AcTCAGCAACTAAATGCAGAATTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAA
 CTTTATTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTC
 CGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAGACAATTGT
 CAAATGAGTCAGACCAAAAGTATGGTAAACTTGT'TTTTATTTAAGGACGGGTAAAA
 AGGACATTTTACTATGATTTTAAAGAAGAACTTAA

SEQ ID NO. 8202

STRAIN 090

AATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTTA
 CGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTT
 CCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGT
 TAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAACTTGT'TTTT
 TATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGA
 AACT

SEQ ID NO. 8203

STRAIN A909

CAGAATTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
 TTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATG
 GGTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTGT'T
 TTTTATTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
 AGAAACT

SEQ ID NO. 8204

STRAIN H36B

ATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTT
 TATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGA
 TGATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTT
 ATGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTT
 GTTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAA
 AGAAGAACT

SEQ ID NO. 8205

STRAIN 18RS21

AGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTTATT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGG
 GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTGT'TT
 TTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAA
 GAACT

SEQ ID NO. 8206

STRAIN M732

CAGAATTGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
 TTTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATG
 GGTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTGT'T
 TTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
 AGAACT

SEQ ID NO. 8207

STRAIN COH1

GAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTT
 ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
 TCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGGG
 TTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTGT'TTT
 TTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAG
 AACT

SEQ ID NO. 8208

STRAIN M781

AGAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGG
 GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTGT'TT
 TTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAA
 GAACT

SEQ ID NO. 8209

STRAIN CJB110

GAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTT
 ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
 TCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGG
 TTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAACTTGT'TTT
 TTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAG
 AACT

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8210

STRAIN 1169NT

TCGAAGGCGCTCACTTGGAAATATTTAAGACAGAACAACTTTATTACGT
 AAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAGATGATTTTCG
 TAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAG
 ACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAACTTGTTTTAT
 TTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGAAAC
 T

SEQ ID NO. 8211

STRAIN JM9130013

TGCAGAAITTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTT
 ATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAGAT
 GATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTA
 TGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTG
 TTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAA
 GAAGAACT

PRETTY of: /biotmp/msa128189.2{*} February 7, 2003 08:19 ..

	1				50
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	atgaaaaatt	tattgttaaa	atgtaaggat	aagaaggtta	aagcatttac
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	acttttagaa	tgtttgtag	cattgggtac	aatcacagga	gctttactag
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	tttatcaagg	actgacaaaa	ttgttggtc	aacagatagt	agtgatgtct
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	151				200
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	tcttccagtc	agtctgaatg	ggtgttatta	actcagcaac	taaATGCaga
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	201				250
msa128189.2{6_18RS21}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CITTATTTAC
msa128189.2{6_2603}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CITTATTTAC
msa128189.2{6_A909}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CITTATTTAC
msa128189.2{6_H36B}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CITTATTTAC

Table 82: Comparative Sequences relating to SAG0165

msa128189.2{6_JM9130013}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_COH1}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_M732}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_M781}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_090}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_CJB110}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_1169NT}	~TcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
Consensus	~*~*****	*****--***	*****	*****	*****
msa128189.2{6_18RS21}	251	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA
msa128189.2{6_2603}	300	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA
msa128189.2{6_A909}		GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA
msa128189.2{6_H36B}		GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA
msa128189.2{6_JM9130013}		GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA
msa128189.2{6_COH1}		GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA
msa128189.2{6_M732}		GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA
msa128189.2{6_M781}		GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA
msa128189.2{6_090}		GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA
msa128189.2{6_CJB110}		GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA
msa128189.2{6_1169NT}		GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA
Consensus		*****	*****	*****	*****
msa128189.2{6_18RS21}	301	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG
msa128189.2{6_2603}		CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG
msa128189.2{6_A909}		CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG
msa128189.2{6_H36B}		CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG
msa128189.2{6_JM9130013}		CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG
msa128189.2{6_COH1}		CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG
msa128189.2{6_M732}		CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG
msa128189.2{6_M781}		CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG
msa128189.2{6_090}		CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG
msa128189.2{6_CJB110}		CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG
msa128189.2{6_1169NT}		CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG
Consensus		*****	*****	*****	*****
msa128189.2{6_18RS21}	351	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA
msa128189.2{6_2603}		AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA
msa128189.2{6_A909}		AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA
msa128189.2{6_H36B}		AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA
msa128189.2{6_JM9130013}		AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA
msa128189.2{6_COH1}		AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA
msa128189.2{6_M732}		AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA
msa128189.2{6_M781}		AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA
msa128189.2{6_090}		AGACAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA
msa128189.2{6_CJB110}		AGACAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA
msa128189.2{6_1169NT}		AGACAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA
Consensus		*****	*****	*~*****	*****
msa128189.2{6_18RS21}	401	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT
msa128189.2{6_2603}		ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT
msa128189.2{6_A909}		ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT
msa128189.2{6_H36B}		ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT
msa128189.2{6_JM9130013}		ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT
msa128189.2{6_COH1}		ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT
msa128189.2{6_M732}		ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT
msa128189.2{6_M781}		ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT
msa128189.2{6_090}		ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT
msa128189.2{6_CJB110}		ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT
msa128189.2{6_1169NT}		ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT
Consensus		*****	*****	*****	*****
msa128189.2{6_18RS21}	451	ACT---			
msa128189.2{6_2603}		ACTtaa			
msa128189.2{6_A909}		ACT---			
msa128189.2{6_H36B}		ACT---			
msa128189.2{6_JM9130013}		ACT---			
msa128189.2{6_COH1}		ACT---			
msa128189.2{6_M732}		ACT---			
msa128189.2{6_M781}		ACT---			
msa128189.2{6_090}		ACT---			
msa128189.2{6_CJB110}		ACT---			
msa128189.2{6_1169NT}		ACT---			
Consensus		*****			

SEQ ID NO. 8212

STRAIN 2603 frame: 1

MKNLLKCKDKKVKAFLLLECLVALVTITGALLVYQGLTKLLAQQIVVMSSSSQSEWVLL
 TQQLNAEFEGAHLEYLRQNKLLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNC

Table 82: Comparative Sequences relating to SAG0165

QMSQTKSMVKLVFYFKDGLKRTFFYDFKEET.

SEQ ID NO. 8213

STRAIN 090 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKS
MVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8214

STRAIN A909 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8215

STRAIN H36B frame: 3

AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8216

STRAIN 18RS21 frame: 2

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8217

STRAIN M732 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8218

STRAIN COH1 frame: 1

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8219

STRAIN M781 frame: 2

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8220

STRAIN CJB110 frame: 1

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8221

STRAIN 1169NT frame: 3

EGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKSM
VKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8222

STRAIN JM9130013 frame: 2

AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFFYDFKEET

PRETTY of: /biotmp/msa128319.2{*} February 7, 2003 08:27 ..

	1				50
msa128319.2{6_090}	-----	-----	-----	-----	-----
msa128319.2{6_1169NT}	-----	-----	-----	-----	-----
msa128319.2{6_18RS21}	-----	-----	-----	-----	-----
msa128319.2{6_2603}	mknlllkckd	kkvkaftlle	clvalvtitg	allvyqgltk	llaqqivvms
msa128319.2{6_H36B}	-----	-----	-----	-----	-----
msa128319.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128319.2{6_A909}	-----	-----	-----	-----	-----
msa128319.2{6_CJB110}	-----	-----	-----	-----	-----
msa128319.2{6_COH1}	-----	-----	-----	-----	-----
msa128319.2{6_M732}	-----	-----	-----	-----	-----
msa128319.2{6_M781}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa128319.2{6_090}	-----	-----fEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_1169NT}	-----	-----EG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_18RS21}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_2603}	sssqsewvll	tqqlnAEfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_H36B}	-----	-----AEfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_JM9130013}	-----	-----AEfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_A909}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_CJB110}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_COH1}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_M732}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_M781}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
Consensus	*****	*****-*	*****	*****	*****

Table 82: Comparative Sequences relating to SAG0165

	101		150
msa128319.2{6_090}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_1169NT}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_18RS21}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_2603}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_H36B}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_JM9130013}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_A909}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_CJB110}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_COH1}	RKTGYnGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_M732}	RKTGYnGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_M781}	RKTGYnGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
Consensus	*****	*****	*****
	151		
msa128319.2{6_090}	T-		
msa128319.2{6_1169NT}	T-		
msa128319.2{6_18RS21}	T-		
msa128319.2{6_2603}	T-		
msa128319.2{6_H36B}	T-		
msa128319.2{6_JM9130013}	T-		
msa128319.2{6_A909}	T-		
msa128319.2{6_CJB110}	T-		
msa128319.2{6_COH1}	T-		
msa128319.2{6_M732}	T-		
msa128319.2{6_M781}	T-		
Consensus	**		

Table 83: Comparative Sequences relating to SAG0108

SEQ ID NO. 8301

STRAIN 2603

atgaaaaagattcgattatcaaagtttattaaaatgattgttgttattttgtttttaatt
 agtgtagcagctagtttttatttttccacgttgcccaagttcgagatgataaatccttt
 atttcaaatgggtcaacgttaagcctggaaactctttatatgtctatgataaatcctttgat
 aagctattaaagcaaaaaatagaaatgacaaacaaaataaaagcaagttgcttggat
 gttcctgctgttaagaaaactcataagacagctgttgcgttcaggttttgcgaatagc
 aaagagaatatgaaggcatatgggttggctgtttcataagttaggatataaatgttcttatg
 cctgacaatattgcacatgggtgaaagtcatgggcagttgataggctatggctggaacgac
 cgcgagaacattatcaaatggacagaaatgatagttgataagaatccatcaagccaaatt
 actttatttgggtgtttcaatgggtggagcaacagtcagtgatggctagtgggtgaaaaatta
 cctagtcaggtgtttaatcatctgaagattgcggttattctagtggttggatgaatta
 aaatttcaggctaaagagatgtatgggttaccagccttcccactcttatatgaagtttca
 acaatttctaaaatcagagcaggttttctgtatggacaagcaagtagtgcgaacaattg
 aaaaagaataatttaccagccctcttattcatggtgataaggataatttgttccaaca
 agtatgggttatgacaactataaagctacagcaggttaagaaagagctttatattgtaaaa
 ggggcaaacatgcgaatcttttgaacagagccagaaaaatagagaaacgtatctct
 agttttttgaaaaaatatgaaaaa

SEQ ID NO. 8302

STRAIN 090

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCC
 AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAATAGAA
 ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAA
 GAAAACTCATAAGACAGCTGTTGTCTGTTTCATGGTTTTGCGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTATGCTGACATATGTCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCAATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTACTTTaTTTGGTGTTCATGGGT
 GGAGCAACAGCTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
 TAATATCATTTGAAGATTGCGGTTATTCTAGTGTTTGGGATGAATTAATA
 TTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCCTCTTATATGAA
 GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTCTGTATGGACAAGCAAG
 TAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATG
 GTGATAAGGATAATTTTGTCCAAAGATATGGTTTATGACAACTATAAAA
 GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAGGGGCAAAACATGC
 GAAATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGA AAAAATATGAAAAA

SEQ ID NO. 8303

STRAIN A909

AATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCT
 TATGATAAATCCTTTGATAAGCTATTAAAGCAAAAATAGAAATGACAAA
 CCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTC
 ATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGAGAATATG
 AAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCC
 TGACAACATTGCAACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCT
 GGAACGACCGCGAAGCAATTTCAAATGGACAGAAATGATAGTTGATAAG
 AATTCTCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGGAGCAAC
 AGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCA
 TTGAAGATGCGGTTATTCTGTTGTTGGGATGAATTAATAATTCAGGCT
 AAAGAGATGTATGGTTTACCAGCCTTCCCCTCTTATATGAAGTTTCAAC
 AATTTCTAAAATCAGAGCAGGTTTTCTGTATGGACAAGCAAGTAGTGTG
 AACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGGTGATAAG
 GATAATTTTGTTCACAAAGTATGGTTTATGACAACTATAAGCTACAGC
 AGGTAAGAAAGAGCTTTATATTGTAAAGGGGCAAAACATGCGAAATCTT
 TTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAA
 AAATATGAAAAA

SEQ ID NO. 8304

STRAIN H36B

AGTTTTTATTTTTTCCACGTTGCCCAAGTTTCGAGATGATAAATCCTTTAT
 TTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCTTATGATAAAT
 CCTTTGATAAGCTATTAAAGCAAAAATAGAAATGACAAACCAAAATATA
 AAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTCATAAGACAGC
 TGTTCGTTTCATGGTTTTGCGAATAGCAAAGAGAATATGAAGGCATATG
 GTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCTGACAACTATG
 GCACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCTGGAACGACCG
 CGAGAACATTATCAAATGGACAGAAATGATAGTTGATAAGAAATTCATCAA
 GCCAAATTACTTTATTTGGTGTTCATGGGTGGAGCAACAGTCATGATG
 GCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCATTTGAAGATTG
 CGGTTATTCTGGTGTTTGGGATGAATTAATAATTCAGGCTAAAGAGATGT
 ATGGTTTACCAGCCTTCCCCTCTTATATGAAGTTTCAACAATTTCTAAA
 ATCAGAGCAGGTTTTCTGTATGGACAAGCAAGTAGTGTGCAACAATTGAA
 AAGAAATAATTTACCAGCCCTCTTTATTCATGGTGATAAGGATAATTTTG
 TTCCAACAAGTATGGTTTATGACAACTATAAGCTACAGCAGGTAAGAAA
 GAGCTTTATATTGTAAAGGGGCAAAACATGCGAAATCTTTTGAACAGA
 GCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAAAATATGAAA
 AA

SEQ ID NO. 8305

STRAIN 18RS21

Table 83: Comparative Sequences relating to SAG0108

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
 ATATGCTTTATGATAAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGTTAAG
 AAAACTCATAAGACAGCTGTTGTCTGTTTCATGGTTTTGCGAATAGCAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTTC
 TTATGCTTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTGCGGTTATTCTAGTGTGGGATGAATTAAAAAT
 TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGG
 TGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
 AAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8306

STRAIN M732

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
 ATATGCTTTATGATAAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGCTAAG
 AAAACTCATAAGACAGTTGTTGTCTGTTTCATGGTTTTGCGAATAGCAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTTC
 TTATGCTTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 GGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTGTTGTTTATTCTAGTGTGGGATGAATTAAAAAT
 TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGG
 TGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
 AAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8307

STRAIN COH1

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTC
 GAGATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCT
 TTATATGCTTTATGATAAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGA
 AATGaCAAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGCTA
 AGAAAACTCATAAGACAGTTGTTGTCTGTTTCATGGTTTTGCGAATAGCAAA
 GAGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGT
 TCTTATGCTTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAG
 CTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATA
 GTGGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 TGGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTG
 TTAATATCATTGAAGATTGTTGTTTATTCTAGTGTGGGATGAATTAAAA
 TTTGAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
 AGTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAA
 GTAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCAT
 GGTGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAA
 AGCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
 CGAAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT
 TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8308

STRAIN M781

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCG
 AGATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTTATGATAAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
 ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGCTAA
 GAAAACTCATAAGACAGTTGTTGTCTGTTTCATGGTTTTGCGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTTATGCTTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAG
 TGGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGTG
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 TAAATATCATTGAAGATTGTTGTTTATTCTAGTGTGGGATGAATTAAAA
 TTTGAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
 GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
 TAgTGTGCAACAATtGAAAAAGAATAATTTACCAGCCCTCTTTATTCATG
 GTGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACCTATAAA
 GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
 GAAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8309

Table 83: Comparative Sequences relating to SAG0108

STRAIN CJB110

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGAG
 ATGATAAATCCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTTTA
 TATGCTTATGATAAATCCCTTTGATAAGCTATTAAAGCAAAAAATAGAAAT
 GACAAACCAAAATATAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGA
 AAACCTATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGAG
 AATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTcT
 TATGCTGTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGCT
 ATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGTT
 GATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGG
 AGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTA
 ATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAAATAAAAATTT
 CAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAGT
 TTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGTA
 gTGTGGAACAATGAAAAAGAAATAATTTACCAGCCCTcTTTATTCATGGT
 GATAAGGATAAATTTGTTTCCAACAAGTATGGTTTATGACAACTATAAAGC
 TACAGCAGGTAAAGAAAGAGCTTTATATTTGTAAGGGGGCAAAACATGCGA
 AATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTT
 TTGAAAAAATATGAAAA

SEQ ID NO. 8310

STRAIN 1169NT

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAATCCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTTT
 ATATGCTTATGATAAATCCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCcAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAG
 AAAACCTATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGA
 gAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTc
 TTATACCTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGCT
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTgCGGTTATTcTAGTGTTTGGGATgAAATAAAAAT
 TCAGGCTAaAGAGATGTATGGTTTaCCAGCCTTCCCACTcTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTAGAACAAATGAAAAAGAAATAATTTACCAGCCCTCTTTATTCATGG
 TGATAAGGATAAATTTGTTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAAGAAAGAGCTTTATATTTGTAAGGGGGCAAAACATGCG
 AATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTT
 TTTGAAAAAATATGAAAA

SEQ ID NO. 8311

STRAIN JM9130013

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
 AGATGATAAATCCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTTT
 TATATGCTTATGATAAATCCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
 ATGaCAAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGTTAA
 GAAAACTATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTATGCTGTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCaAATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGT
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
 TAATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAAATAAAAAT
 TTCAAGCTAaAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
 TAGTGTGGAACAATGAAAAAGAAATAATTTACCAGCCCTCTTTATTCATG
 GTGATAAGGATAAATTTGTTTCCAACAAGTATGGTTTATGACAACTATAAA
 GCTACAGCAGGTAAAGAAAGAGCTTTATATTTGTAAGGGGGCAAAACATGCG
 GAAATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGAAAAAATATGAAAA

PRETTY of: /biotmp/msa286608.2{*} February 24, 2003 06:26 ..

	1				50
msa286608.2{662_COH1}	-----	-----	-----	-----	-----
msa286608.2{662_M732}	-----	-----	-----	-----	-----
msa286608.2{662_M781}	-----	-----	-----	-----	-----
msa286608.2{662_A909}	-----	-----	-----	-----	-----
msa286608.2{662_H36B}	-----	-----	-----	-----	-----
msa286608.2{662_090}	-----	-----	-----	-----	-----
msa286608.2{662_CJB110}	-----	-----	-----	-----	-----
msa286608.2{662_18RS21}	-----	-----	-----	-----	-----
msa286608.2{662_2603}	atgaaaaaga	ttcgattatc	aaagtttatt	aaaatgattg	ttgtattttt
msa286608.2{662_JM9130013}	-----	-----	-----	-----	-----
msa286608.2{662_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa286608.2{662_COH1}	-----	-----g	ctagttttta	ttttttccac	gttgcccaag
msa286608.2{662_M732}	-----	-----g	ctagttttta	ttttttccac	gttgcccaag
msa286608.2{662_M781}	-----	-----g	ctagttttta	ttttttccac	gttgcccaag

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_A909}	-----	-----	-----	-----	-----
msa286608.2{662_H36B}	-----	-----	agtttttta	ttttttccac	gttgcccaag
msa286608.2{662_090}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_CJB110}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_18RS21}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_2603}	gtttttaatt	agtgttagcag	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_JM9130013}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_1169NT}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
Consensus	*****	*****	-----	-----	-----
101					
msa286608.2{662_COH1}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_M732}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_M781}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_A909}	-----	AAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_H36B}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_090}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_CJB110}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_18RS21}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_2603}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_JM9130013}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
msa286608.2{662_1169NT}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC
Consensus	-----	*****	*****	*****	*****
151					
msa286608.2{662_COH1}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_M732}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_M781}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_A909}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_H36B}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_090}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_CJB110}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_18RS21}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_2603}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_JM9130013}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_1169NT}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
Consensus	*****	*****	*****	*****	*****
201					
msa286608.2{662_COH1}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_M732}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_M781}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_A909}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_H36B}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_090}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_CJB110}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_18RS21}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_2603}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_JM9130013}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_1169NT}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
Consensus	*****	*****	*****	*****	*****
251					
msa286608.2{662_COH1}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_M732}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_M781}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_A909}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_H36B}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_090}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_CJB110}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_18RS21}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_2603}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_JM9130013}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_1169NT}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
Consensus	*****	*****	*****	*****	*****
301					
msa286608.2{662_COH1}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_M732}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_M781}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_A909}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_H36B}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_090}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_CJB110}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_18RS21}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_2603}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_JM9130013}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_1169NT}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
Consensus	*****	*****	*****	*****	*****
351					
msa286608.2{662_COH1}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_M732}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
400					

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_M781}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_A909}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_H36B}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_090}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_CJB110}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_18RS21}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_2603}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_JM9130013}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_1169NT}	TGTTCTTATa	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
Consensus	*****-*****	*****	*****	*****	*****
msa286608.2{662_COH1}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_M732}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_M781}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_A909}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_H36B}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_090}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_CJB110}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_18RS21}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_2603}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_JM9130013}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_1169NT}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_M732}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_M781}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_A909}	ATAGTtGATA	AGAATtCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_H36B}	ATAGTtGATA	AGAATtCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_090}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_CJB110}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_18RS21}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_2603}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_JM9130013}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_1169NT}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_M732}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_M781}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_A909}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_H36B}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_090}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_CJB110}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_18RS21}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_2603}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_JM9130013}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_1169NT}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_M732}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_M781}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_A909}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTgGTGTTTg	GGATGAATTA
msa286608.2{662_H36B}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTgGTGTTTg	GGATGAATTA
msa286608.2{662_090}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_CJB110}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_18RS21}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_2603}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_JM9130013}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_1169NT}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
Consensus	*****	*****	**..*****	**..*****	*****
msa286608.2{662_COH1}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_M732}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_M781}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_A909}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_H36B}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_090}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_CJB110}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_18RS21}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_2603}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_JM9130013}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_1169NT}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_M732}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_M781}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_A909}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_H36B}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_090}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_CJB110}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_18RS21}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_2603}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_JM9130013}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_1169NT}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_M732}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_M781}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_A909}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_H36B}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_090}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_CJB110}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_18RS21}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_2603}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_JM9130013}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
msa286608.2{662_1169NT}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTATT
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_M732}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_M781}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_A909}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_H36B}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_090}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_CJB110}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_18RS21}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_2603}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_JM9130013}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_1169NT}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_M732}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_M781}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_A909}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_H36B}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_090}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_CJB110}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_18RS21}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_2603}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_JM9130013}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_1169NT}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_M732}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_M781}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_A909}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_H36B}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_090}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_CJB110}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_18RS21}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_2603}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_JM9130013}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_1169NT}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_M732}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_M781}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_A909}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_H36B}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_090}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_CJB110}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_18RS21}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_2603}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_JM9130013}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_1169NT}	AGTTTTTTGA	AAAAATATGA	AAAA		
Consensus	*****	*****	*****		

Table 83: Comparative Sequences relating to SAG0108

STRAIN 2603 frame: 1

MKKIRLSKFIKMIIVILFLISVAASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFD
KLLKQKIEMTNQNIKQVAVYVPAVKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLM
PDNIAHGESHGQLIGYWNDRNI IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKL
PSQVVNI IEDCGYSSVWDELKFKQAKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQL
KKNNLPALFIHGDKNFVPTSMVYDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8313

STRAIN 090 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNNLPALFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8314

STRAIN A909 frame: 3

SFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPAKKTHKTAVVHGF
NSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI IKWTEMIVDKNSS
QITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSGVWDELKFKQAKEMYGLPAFPLLYE
VSTISKIRAGFSYQGASSVEQLKKNNLPALFIHGDKNFVPTSMVYDNYKATAGKKELYI
VKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8315

STRAIN H36B frame: 1

SFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
KTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSGVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNNLPALFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8316

STRAIN 18RS21 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
VKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNNLPALFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8317

STRAIN M732 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNNLPALFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8318

STRAIN COH1 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNNLPALFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8319

STRAIN M781 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNNLPALFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8320

STRAIN CJB110 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNNLPALFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8321

STRAIN 1169NT frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLI PDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNNLPALFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8322

Table 83: Comparative Sequences relating to SAG0108

STRAIN JM9130013 frame: 1

ASFFYFFHVAQVRDDKSF ISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
 VKKTHKTAVVVHGFANSKENMKAYGWL FHLKGYNVLM PDNIAHGESHGQLIGYGWNDREN
 I IKWTEMI VDKNPSSQITLFGVSMGGATVMMASGEKLP SQVVNI I EDCGYSVWDELKFO
 AKEMYGLPAFPLLYEVSTISKIRAGFSYQASSVEQLKKNLPALEI HGDKNFVPTSMV
 YDNYKATAGKKELYIVKAKHAKSFETEPEKYEKRIS SFLKKYK

PRETTY of: /biotmp/msa286876.2{*} February 24, 2003 06:46 ..

	1				50
msa286876.2{662_A909}	-----	-----	-----	-----SF	ISNGQRKPGN
msa286876.2{662_H36B}	-----	-----	---SFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_COH1}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_M732}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_M781}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_18RS21}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_2603}	mkkirlskfi	kmivvilfli	svaASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_JM9130013}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_090}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_CJB110}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_1169NT}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
Consensus	*****	*****	*****	*****	*****
	51				100
msa286876.2{662_A909}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_H36B}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_COH1}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_M732}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_M781}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_18RS21}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_2603}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_JM9130013}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_090}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_CJB110}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_1169NT}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
Consensus	*****	*****	*****	*****	*****
	101				150
msa286876.2{662_A909}	KENMKAYGWL	FHLKGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_H36B}	KENMKAYGWL	FHLKGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_COH1}	KENMKAYGWL	FHLKGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_M732}	KENMKAYGWL	FHLKGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_M781}	KENMKAYGWL	FHLKGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_18RS21}	KENMKAYGWL	FHLKGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_2603}	KENMKAYGWL	FHLKGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_JM9130013}	KENMKAYGWL	FHLKGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_090}	KENMKAYGWL	FHLKGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_CJB110}	KENMKAYGWL	FHLKGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_1169NT}	KENMKAYGWL	FHLKGYNVLM	PDNIAHGESH	GQLIGYGWND	RENI IKWTEM
Consensus	*****	*****	*****	*****	*****
	151				200
msa286876.2{662_A909}	IVDKNsSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSgVWDEL
msa286876.2{662_H36B}	IVDKNsSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSgVWDEL
msa286876.2{662_COH1}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_M732}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_M781}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_18RS21}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_2603}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_JM9130013}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_090}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_CJB110}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_1169NT}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
Consensus	*****	*****	*****	*****	*****
	201				250
msa286876.2{662_A909}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_H36B}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_COH1}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_M732}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_M781}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_18RS21}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_2603}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_JM9130013}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_090}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_CJB110}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_1169NT}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
Consensus	*****	*****	*****	*****	*****
	251				300
msa286876.2{662_A909}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_H36B}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_COH1}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS

Table 83: Comparative Sequences relating to SAG0108

msa286876.2{662_M732}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_M781}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_18RS21}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_2603}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_JM9130013}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_090}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_CJB110}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_1169NT}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
Consensus	*****	*****	*****	*****	*****
301					
msa286876.2{662_A909}	SFLKKYEK				
msa286876.2{662_H36B}	SFLKKYEK				
msa286876.2{662_COH1}	SFLKKYEK				
msa286876.2{662_M732}	SFLKKYEK				
msa286876.2{662_M781}	SFLKKYEK				
msa286876.2{662_18RS21}	SFLKKYEK				
msa286876.2{662_2603}	SFLKKYEK				
msa286876.2{662_JM9130013}	SFLKKYEK				
msa286876.2{662_090}	SFLKKYEK				
msa286876.2{662_CJB110}	SFLKKYEK				
msa286876.2{662_1169NT}	SFLKKYEK				
Consensus	*****				

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8401

STRAIN 2603

ATGATGAAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACTAAAC
 AATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAAATCATAGCATTAAATTG
 ATGCCAGCCATTGATTTTAAATGCAATCAATTGATTAGAACCCTCAAGATTGGACCGT
 ATCGTAGTAGCAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTACAGCA
 AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTA
 ACAAATGGATTTTCAGAAAATGATTTATTGGTACCCTTATAGATGCACGACGTAATAAT
 GTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAGACTGTACACTTCTCTT
 GAAGAAGTCTTACAAGAGGTGGGGAATAAAGCCAATGTTTATTGTCGGAGAGGTTGCA
 GCATTTTGTGATCAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAAACCTTTACCT
 TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATGCGTTT
 GTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTGTGAA
 ACGAATACAGAAGAAATATATTAAAGAGAGTT

SEQ ID NO. 8402

STRAIN 090

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACT
 AAACAATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAAATC
 ATAGCATTAAATTGATGCCAGCCATTGATTTTAAATGCAATCAATTGAT
 TTAGAACCCTCAAGATTGGACCGTATCGTAGTGGCAGAGGGTCCAGGATC
 TTATACGGGCTTACGTGTAGCTGTTGTACAGCAAAAATGCTAGCTTATA
 CGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTAAACAAT
 GGATTTTCAGAAAATGATTTGTTGGTACCCTTATAGATGCACGACGTAA
 CAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAGACT
 GTACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGAATAAAGCCAAT
 GTTCATTTTGTGCGAGAGGTTGCAGCATTTTGTGATCAGATTAAAGAAAGC
 CTTACCACATGCTAAAATTACAGAAACCTTTACCTTGTGCAGTGGCAATTG
 GCGCAAGAGGACAAAAATGGAAGCGTTAATGTAGATGCGTTTGTTCAC
 CGATACTTAAAACGAGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTG
 TGAACGAAT

SEQ ID NO. 8403

STRAIN A909

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAG
 TGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATATC
 AAAAAAGAAATCATAGCATTAAATTGATGCCAGCCATTGATTTTAAATGCA
 ATCAATTGATTAGAACCCTCAAGATTGGACCGTATCGTAGTAGCAGAGG
 GTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTCTACAGCAAAAATG
 CTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGC
 TTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCCTTATAGATG
 CACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGTT
 AAACCAGACTGTACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 TAAAGCCAATGTTTATTTGTGCGAGAGGTTGCAGCATTTGTTGACCAGA
 TTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 GCGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATGC
 GTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTAA
 GAAACCACTGTGAACGAAT

SEQ ID NO. 8404

STRAIN H36B

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAAATCATAGCATTAAATTGATGCCAGCCATTGATTTTAAATGC
 AATCAATTGATTAGAACCCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
 TAAACCAAGCTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTATTTGTGCGAGAGGTTGCAGCATTTGTTGACCAG
 ATTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
 AGAAACCACTGTGAACGAATACAGAAGAAATATATTAAAGAGAGTT

SEQ ID NO. 8405

STRAIN 18RS21

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAAATCATAGCATTAAATTGATGCCAGCCATTGATTTTAAATGC
 AATCAATTGATTAGAACCCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
 TAAACCAAGCTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTATTTGTGCGAGAGGTTGCAGCATTTTGTGATCAG
 ATTAAGAAAGCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 AGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
 AGAAACCACTGTGAACGAATACAGAAGAAATATATTAAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8406

STRAIN M732

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGACTGT
 TAAACCAAGCTGTACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTGATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGAnn
 CGTTTGTTCACGATACCTTAAACGTTGTAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8407

STRAIN COH1

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCAC
 TATCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATC
 AATATCAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTT
 AATGCAATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAG
 CAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCA
 AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCT
 GTACGCTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACCTTA
 TAGATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGAT
 ACTGTTAAACCAAGCTGTACACTTCTCTTGAAGAAGTCTTACAAGAGGT
 GGGGAATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTG
 ATCAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCT
 TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGT
 AGATGCGTTTGTTCACGATACCTTAAACGTTGTAAGCTGAGGAAAATT
 GGTAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8408

STRAIN M781

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTA
 TCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAA
 TATCAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAA
 TGCAATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTATCA
 GAGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAA
 AATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGT
 ACGCTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACCTTATA
 GATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATAC
 TGTTAAACCAAGCTGTACACTTCTCTTGAAGAAGTCTTACAAGAGGTGG
 GGAATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTGAT
 CAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGT
 TGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAG
 ATGCGTTTGTTCACGATACCTTAAACGTTGTAAGCTGAGGAAAATTGGTTA
 TAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8409

STRAIN CJB110

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTGCCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTGTTGGTACCACCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGACTGT
 TAAACCAAGCTGTACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTgATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACCTTAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8410

STRAIN I169NT

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGACTGT
 TAAACCAAGCTGTACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTgATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACCTTAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267

AGTGGCAATTGGGCGCAAAGGACAAAAATGGAAGCGTTAATGTAGATG
CGTTTGTTCACGATACCTTAAACGTGTTGAAGCTGAGGAAATTTGGTTA
AAAAACCACTGTGAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO.: 8411

STRAIN JM9130013

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTAATGC
AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAT
gCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAATATGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
TAAACCAAGCTGTCACTTCTCTTGAAGAAGCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTTCAATTTTGTTCGAGAGGTTGCAGCATTGTTGACCAG
ATTAAGAAAGTTTACCAATGCTTAAATTACAGAAACCTTACCTTTGTGC
AGTGGCAATTGGGCGCAAAGGACAAAAATGGAAGCGTTAATGTAGATG
CGTTTGTTCACGATACCTTAAACGTGTTGAAGCTGAGGAAATTTGGTTA
AGAAACCACTGTGAACGAATACAGAAGAATATATTAAAGAGAGTT

PRETTY of: /biotmp/msa521675.2{*} March 10, 2003 08:34 ..

	1		50
msa521675.2{69_A909}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_H36B}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_JM9130013}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_1169NT}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_090}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_CJB110}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_18RS21}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_2603}	atgatgAAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_COH1}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_M732}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_M781}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
Consensus	*****	*****	*****

	51		100
msa521675.2{69_A909}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_H36B}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_JM9130013}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_1169NT}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_090}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_CJB110}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_18RS21}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_2603}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_COH1}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_M732}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_M781}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
Consensus	*****	*****	*****

	101		150
msa521675.2{69_A909}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_H36B}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_JM9130013}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_1169NT}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_090}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_CJB110}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_18RS21}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_2603}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_COH1}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_M732}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_M781}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
Consensus	*****	*****	*****

	151		200
msa521675.2{69_A909}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_H36B}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_JM9130013}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_1169NT}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_090}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_CJB110}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_18RS21}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_2603}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_COH1}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_M732}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_M781}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
Consensus	*****	*****	*****

	201		250
msa521675.2{69_A909}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT TGCTACAGCA AAAATGCTAG
msa521675.2{69_H36B}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT TGCTACAGCA AAAATGCTAG

Table 84: Comparative Sequences relating to SAG0267

msa521675.2{69_JM9130013}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_1169NT}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_090}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_CJB110}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_18RS21}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_2603}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_COH1}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_M732}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_M781}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
Consensus	*****	*****	*****	*****	*****
251					
msa521675.2{69_A909}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_H36B}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_JM9130013}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_1169NT}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_090}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_CJB110}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_18RS21}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_2603}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_COH1}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_M732}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_M781}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
Consensus	*****	*****	*****	*****	*****
301					
msa521675.2{69_A909}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_H36B}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_JM9130013}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_1169NT}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_090}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_CJB110}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_18RS21}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_2603}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_COH1}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_M732}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_M781}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
Consensus	*****	*****	*****-***	*****	*****
351					
msa521675.2{69_A909}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_H36B}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_JM9130013}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_1169NT}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_090}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_CJB110}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_18RS21}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_2603}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_COH1}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_M732}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_M781}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
Consensus	*****-***	*****	*****	*****-***	*****
401					
msa521675.2{69_A909}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_H36B}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_JM9130013}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_1169NT}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_090}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_CJB110}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_18RS21}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_2603}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_COH1}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_M732}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_M781}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
Consensus	*****	*****	*****	*****	*****
451					
msa521675.2{69_A909}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_H36B}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_JM9130013}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_1169NT}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_090}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_CJB110}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_18RS21}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_2603}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_COH1}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_M732}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_M781}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
Consensus	*****	*****	*****	*****-***	*-*****
501					
msa521675.2{69_A909}	GAAAGtTTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
550					

Table 84: Comparative Sequences relating to SAG0267

msa521675.2{69_H36B}	GAAAGcttTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_JM9130013}	GAAAGcttTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_1169NT}	GAAAGcttTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_090}	GAAAGccTtA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_CJB110}	GAAAGccTtA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_18RS21}	GAAAGccTtA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_2603}	GAAAGccTtA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_COH1}	GAAAGccTtA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_M732}	GAAAGccTtA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_M781}	GAAAGccTtA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
Consensus	*****-***	*****	*****	*****	*****
msa521675.2{69_A909}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_H36B}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_JM9130013}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_1169NT}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_090}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_CJB110}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_18RS21}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_2603}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_COH1}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_M732}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_M781}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
Consensus	*****	*****	*****-***	*****	*****
msa521675.2{69_A909}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_H36B}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_JM9130013}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_1169NT}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_090}	GTTCACGAT	ACTTAAAACG	aGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_CJB110}	GTTCACGAT	ACTTAAAACG	aGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_18RS21}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_2603}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_COH1}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_M732}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_M781}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
Consensus	*****	*****	-*****	*****	*****-***
msa521675.2{69_A909}	CCACTGTGAA	ACGAAT----	-----	-----	690
msa521675.2{69_H36B}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_JM9130013}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_1169NT}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_090}	CCACTGTGAA	ACGAAT----	-----	-----	
msa521675.2{69_CJB110}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_18RS21}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_2603}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_COH1}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_M732}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_M781}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
Consensus	*****	*****	*****	*****	

SEQ ID NO. 8412

STRAIN 2603 frame: 1

MMKVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDR
 IVVAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENLLVPLIDARRNN
 VYVGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 CAVAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETNTTEEYIKRV

SEQ ID NO. 8413

STRAIN 090 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETN

SEQ ID NO. 8414

STRAIN A909 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETN

SEQ ID NO. 8415

STRAIN H36B frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETNTTEEYIKRV

SEQ ID NO. 8416

Table 84: Comparative Sequences relating to SAG0267

STRAIN 18RS21 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEABENWLKNHCETNTEEYIKRV

SEQ ID NO. 8417

STRAIN M732 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVXXFVPRYLKRVEABENWLKNHCETNTEEYIKRV

SEQ ID NO. 8418

STRAIN COH1 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEABENWLKNHCETNTEEYIKRV

SEQ ID NO. 8419

STRAIN M781 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VSEGPSTYGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEABENWLKNHCETNTEEYIKRV

SEQ ID NO. 8420

STRAIN CJB110 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEABENWLKNHCETNTEEYIKRV

SEQ ID NO. 8421

STRAIN 1169NT frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEABENWLKNHCETNTEEYIKRV

SEQ ID NO. 8422

STRAIN JM9130013 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEABENWLKNHCETNTEEYIKRV

PRETTY of: /biotmp/msa521982.2{*} March 10, 2003 08:40 ..

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1                                     50
msa521982.2{69_A909} --KVLAFTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_H36B} --KVLAFTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_JM9130013} --KVLAFTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_090} --KVLAFTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_CJB110} --KVLAFTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_18RS21} --KVLAFTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_2603} --KVLAFTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_COH1} --KVLAFTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_M781} --KVLAFTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_1169NT} --KVLAFTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_M732} --KVLAFTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
Consensus *****
51                                     100
msa521982.2{69_A909} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_H36B} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_JM9130013} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_090} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_CJB110} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_18RS21} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_2603} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_COH1} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M781} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_1169NT} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M732} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
Consensus *****
101                                     150
msa521982.2{69_A909} TNGFSENDLL VPLIDARRNN VYVGIFYQNGD TVKPDCHTSL EEVLQEVGNK
msa521982.2{69_H36B} TNGFSENDLL VPLIDARRNN VYVGIFYQNGD TVKPDCHTSL EEVLQEVGNK

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Table 84: Comparative Sequences relating to SAG0267

msa521982.2{69_JM9130013}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_090}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_CJB110}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_18RS21}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_2603}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_COH1}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_M781}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_1169NT}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_M732}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
Consensus	*****	*****	*****	*****	*****
151					
msa521982.2{69_A909}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_H36B}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_JM9130013}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_090}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_CJB110}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_18RS21}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_2603}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_COH1}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_M781}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_1169NT}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_M732}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVxxF
Consensus	*****	**_*****_*	*****	*****	**_*****_*
201					
msa521982.2{69_A909}	VPRYLKRVEA	EENWLrNHCE	TN-----	230	
msa521982.2{69_H36B}	VPRYLKRVEA	EENWLrNHCE	TNTEEYIKRV		
msa521982.2{69_JM9130013}	VPRYLKRVEA	EENWLrNHCE	TNTEEYIKRV		
msa521982.2{69_090}	VPRYLKRVEA	EENWLkNHCE	TN-----		
msa521982.2{69_CJB110}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_18RS21}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_2603}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_COH1}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_M781}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_1169NT}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_M732}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
Consensus	*****	*****	*****		

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8501

STRAIN 2603

atgagtaaaccgacaaaatttaggaattagtaaaaaaggagcaattatatcagggtctctca
 gtggcactaattgtagtaaataggtgggtttttatgggtacaatctcaacctaatagagt
 gcagtaaaaactaactacaaagtttttatgttagagaaggaggtgttcgtcctcaact
 cttttgacaggaaggctaaaggctaatcaagaacagtatgtgtattttgatgctaataaa
 ggtaatcgagcaactgtcacagttaaagtgggtgataaaatcacagctgggtcagcagtta
 gttcaabatgatacaacaactgcacaagcagcctacgacactgctaatacgtcaattaaat
 aaagttagcgcgtcagattataatctaagacacaggaagtctccagctatggaatca
 agtgatcaatctcttcatcatcacaaaggacaagggaactcaatcgactagtggtgagcag
 aatcgctctacagcaaaattatcaaagtcaagctaagtctcatacaaccaacaactcaa
 gatgttgatgatgcttatgcagatgcacagcgagaaagtaataaagcacaacaaagcattg
 aatgatactgttattacaagtgcgtatcagggacagttgtgaagttaatagtgatatt
 gatccagcttcaaaaactagtcaggtactgttccatgtgacaaactgaaggtaaaactcaa
 gtacaaggaaacgatgagtgagtgatgtttggctaatgttaaaaaagaccaggctgttaaa
 ataaaatctaaggtctatcctgacaaggaatgggaaggtaaaaatttcatatctcaaat
 tatccagaagcagaagcaacaacaatgactctaataacgggtctagtgtgttaaatat
 aaatataaagtagatattactagccctctcgatgcattaaaacaagggtttaccgtatca
 gttgaagtagtttaaggagataagcaccttatgtccctacaagtctgtgataaaacaaa
 gataataaacactttgttgggtatacaatgattctaatcgtaaaatttccaaagttgaa
 gtcaaaattggtaagctgtagtgaagacacaagaattttatcaggttgaagcagga
 caaatcggtggttactaatccaagtaaaccttcaaggatgggcaaaaattgataatatt
 gaatcaatcgatcttaactctaataagaatcagaggtgaaa

SEQ ID NO. 8502

STRAIN 090

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAGGTAATCGAGCAACTGTCAAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACACGTCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
 ATCATACAAGGACAAGGACTCAATCGACTAGTGGTGGCAGCAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAAACTT
 CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAATAAAGC
 ACAAAAAGCATTTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTCAAGTA
 CTTGTCATGTAGCAACTGAAGGTAAGTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTTAAAAAGACCAAGGCTGTTAAATAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAAAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATGTCTCCTACAAGTTCTGTGATAAAACAAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
 GGACAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAACCTAATAAGAAATCAGAGG

SEQ ID NO. 8503

STRAIN A909

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAA
 CTACAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTT
 TGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCT
 AATAAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCAC
 AGCTGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCT
 ACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAAT
 CTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTC
 ATCATCATACAAGGACAAGGGCTCAATCGACTAGTGGTGGCAGCAATC
 GTCTACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAA
 CTTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAATAA
 AGCACAAAAGCATTTGAATGATACTGTTATTACAAGTGACGTATCAGGGA
 CAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTCAAGTCA
 GTACTTGTCCATGTAGCAACTGAGGGTAAACTCCAAGTACAAGGAACGAT
 GAGTGATATGATTTGGCTAATGTTAAAAAGACCAAGTCTGTTAAATAA
 AATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTATATATC
 TCAAATTATCCAGAAGCAGAAGCAAAACAATGACTCTAATAACGGCTC
 TAGTGCTGTAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATG
 CATTAAAAACAAGGTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAG
 CACCTTATGTTCTTACAAGTTCTGTGACAAAACAAAGATAATAAACACTT
 TGTTTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCA
 AAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAG
 GCAGGACAAATCGTGGTTACTAATCCAAGCAAACTTCAAGGATGGGCA
 AAAAATTGATAATATTGAATCAATAGATCTTAAGTCTAATAAGAAATCAG
 AGGTGAAA

SEQ ID NO. 8504

STRAIN H36B

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC

Table 85: Comparative Sequences relating to SAG1361

TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACACCTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGAAGTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAAACCAACTT
 CAAGATTGGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATCTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATGTATCCAGCTTCAAAAAGTCAAGTA
 CTGTGTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTAAAAAAGACCAGGCTGTTAAATAAAAT
 CTAAGGCTATCTCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
 AATTATCCAGAAGCAGAAGCAACCAACATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTATTTGTTCTTACAAGTTCTGTGACAAACAAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTAGTTACTAATCCAAGTAAAGCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TG

SEQ ID NO. 8505

STRAIN 18RS21

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGAGTAAAACTAACTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACACCTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCTTC
 ATCATCACAAGGACAAGGGAAGTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAAACCAACTT
 CAAGATTGGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATGCTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATGTATCCAGCTTCAAAAAGTCAAGTA
 CTGTGTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTAAAAAAGACCAGGCTGTTAAATAAAAT
 CTAAGGCTCTATCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
 AATTATCCAGAAGCAGAAGCAACCAACATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTATTTGTCCTTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAG

SEQ ID NO. 8506

STRAIN M732

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGAGTAAAACTAATTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACACCTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAAACAGGGAGTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGAAGTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAAACCAACTT
 CAAGATTGGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATGCTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATGTATCCAGCTTCAAAAAGTCAAGTA
 CTGTGTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTAAAAAAGATCAGGCTGTTAAATAAAAT
 CTAAGGCTCTATCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
 AATTATCCAGAAGCAGAAGCAACCAACATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTATTTGTCCTTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TGAA

SEQ ID NO. 8507

STRAIN COH1

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGAGTAAAAAC
 TAATTACAAGTTTAAATGTTAGAGAAGGAAGTGTTCGTCTCAACTC
 TTTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTGAT
 GCTAATAAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAAT
 CACAGCTGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAG
 CTTACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAAT
 AATCTAAAGACAACAGGAGTTTTCAGCTATGGAATCAAGTGATCAATC

Table 85: Comparative Sequences relating to SAG1361

TTCATCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGA
ATCGTCTACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAA
CAACTTCAAAGATTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAA
TAAAGCACAAAAGCATTTGAATGATACTGTTATTACAAGTGACGTATCAG
GGACAGTTGTTGAAGTTAATAGTGATTTGATCCAGCTTCAAAAAGTAGT
CAAGTACTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAAC
GATGAGTGAGTATGATTGGCTAATGTTAAAAAAGATCAGGCTGTTAAAA
TAAAAATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTATAT
ATCTCAAATTTATCCAGAAGCAGAAGCAACAACATGACTCTAATAACGG
CTCTAGTGTCTGTAATTTATAAATATAAAGTAGATATTACTAGCCCTCTCG
ATGCATTAAAAACAGGTTTACCCTGATCAGTTGAAGTAGTTAATGGAGAT
AAGCACCTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACA
CTTTGTTTGGGTATACAATGATTTCTAATCGTAAAAATTTCCAAGTTGAAG
TCAAAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTG
AAAGCAGGACAAATCGTGGTTACTAATCCAAGCAAACTTTCAAGGATGG
GCAAAAAATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAAT
CAGAGGTGAA

SEQ ID NO. 8507

STRAIN M781

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTTGTATGCTAAT
AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAATAAAGTAGCGCTCAGATTAAATAATCTA
AAGACAACAGGGAGTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
ATCATCACAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCT
CAAGATTTGAATGATGCTTATGTCAGATGCACAGGCAGAAAGTAAATAAAGC
ACAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATTTGATCCAGCTTCAAAAAGTAGTCAAGTA
CTTGTCATGATGACCACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGATCAGGCTGTTAAAAATAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTATATATCTCA
AATTATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAATTTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAACCAAGTTTTTACCCTGATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACAACCTTGT
TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTGGTTACTAATCCAAGCAAACTTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TGAA

SEQ ID NO. 8508

STRAIN CJB110

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTTGTATGCTAAT
AAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAATAAAGTAGCGCTCAGATTAAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
ATCATCACAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCT
CAAGATTTGAATGATGCTTATGTCAGATGCACAGGCAGAAAGTAAATAAAGC
ACAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATTTGATCCAGCTTCAAAAAGTAGTCAAGTA
CTTGTCATGATGACCACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGACAGGCTGTTAAAAATAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTATATATCTCA
AATTATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAATTTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAACCAAGGTTTTTACCCTGATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACAACCTTGT
TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTGGTTACTAATCCAAGTAAACCTTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TGA

SEQ ID NO. 8509

STRAIN 1169NT

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACT
AACTACAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCT
TTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTTGAATG
CTAATAAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATC
ACAGCTGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGC
CTACGACACTGCTAATCGTCAATTAATAAAGTAGCGCTCAGATTAAATA
ATCTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCT
TCTTCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAA
TCGCTCTACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAAC

Table 85: Comparative Sequences relating to SAG1361

AACTTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAAT
 AAAGCACAAAAGCATTGAATGATCTGTTATTACAAGTGACGTATCAGG
 GACAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTAGTC
 AAGTACTTGTCCATGTAGCACTGAAGGTAACTCCAAGTACAAGGAACG
 ATGAGTGAGTATGATTTGGCTAATGTTAAAAAGACCAGGCTGTTAAAT
 AAAATCTAAGGTCTATCTGACAAGGAATGGGAAGGTAAATTTTCATATA
 TCTCAAATTATCCAGAAGCAGAAGCAACCAATGACTCTAATAACGGC
 TCTAGTGTGTAATTTAATAATAAAGTAGATATTACTAGCCCTCTCGA
 TGCATTAAAACAAGGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATA
 AGCACCTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAACAC
 TTTGTTTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGT
 CAAAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGA
 AAGCAGGACAAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGG
 CAAAAAATTGATAATATTGAATCAATCGATCTTAACTCTAATAAGAAATC
 AGAGGTGAA

SEQ ID NO. 8510

STRAIN JM9130013

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACACAACCTGCACAAGCAGCCTACG
 ACACGTCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGCTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
 CAAGATTGGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAATAAAGC
 ACAAAGAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTCAAGTA
 CTTGTCCATGTAGCAACTGAGGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAAAGACCAGTCTGTTAAAAATAAAT
 CTAAGGTCTATCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
 AATTATCCAGAAGCAGAAGCAACACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTAATAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGGTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATGTGTTCTTACAAGTTCTGTGACAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGTTAAAGCTGATGCTTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
 GGACAAATCGTGGTTACTAATCCAAGCAAACTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATAGATCTTAAAGTCTAATAAGAAATCAGAGG
 TGAAA

PRETTY of: /biotmp/msa363690.2{*} March 31, 2003 07:01 ..

	1					50
msa363690.2{690_COH1}	-----	-----	-----	-----	-----	-----
msa363690.2{690_M732}	-----	-----	-----	-----	-----	-----
msa363690.2{690_M781}	-----	-----	-----	-----	-----	-----
msa363690.2{690_090}	-----	-----	-----	-----	-----	-----
msa363690.2{690_CJB110}	-----	-----	-----	-----	-----	-----
msa363690.2{690_1169NT}	-----	-----	-----	-----	-----	-----
msa363690.2{690_18RS21}	-----	-----	-----	-----	-----	-----
msa363690.2{690_2603}	atgagtaaac	gacaaaattt	aggaattagt	aaaaaaggag	caattatatac	
msa363690.2{690_A909}	-----	-----	-----	-----	-----	-----
msa363690.2{690_JM9130013}	-----	-----	-----	-----	-----	-----
msa363690.2{690_H36B}	-----	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****	*****

	51					100
msa363690.2{690_COH1}	-----	-----	-----	-----TTT	TTATGGGTAC	
msa363690.2{690_M732}	-----	-----	-----	-----TTT	TTATGGGTAC	
msa363690.2{690_M781}	-----	-----	-----	-----TTT	TTATGGGTAC	
msa363690.2{690_090}	-----	-----	-----	-----TTT	TTATGGGTAC	
msa363690.2{690_CJB110}	-----	-----	-----	-----TTT	TTATGGGTAC	
msa363690.2{690_1169NT}	-----	-----	-----	-----TTT	TTATGGGTAC	
msa363690.2{690_18RS21}	-----	-----	-----	-----TTT	TTATGGGTAC	
msa363690.2{690_2603}	agggctctca	gtggcactaa	ttgtagtaaat	aggtggcTTT	TTATGGGTAC	
msa363690.2{690_A909}	-----	-----	-----	-----TTT	TTATGGGTAC	
msa363690.2{690_JM9130013}	-----	-----	-----	-----TTT	TTATGGGTAC	
msa363690.2{690_H36B}	-----	-----	-----	-----TTT	TTATGGGTAC	
Consensus	*****	*****	*****	*****	*****	*****

	101					150
msa363690.2{690_COH1}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAATACAA	AGTTTTTTAAT	
msa363690.2{690_M732}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAATACAA	AGTTTTTTAAT	
msa363690.2{690_M781}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAATACAA	AGTTTTTTAAT	
msa363690.2{690_090}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAATACAA	AGTTTTTTAAT	
msa363690.2{690_CJB110}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAATACAA	AGTTTTTTAAT	
msa363690.2{690_1169NT}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAATACAA	AGTTTTTTAAT	
msa363690.2{690_18RS21}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAATACAA	AGTTTTTTAAT	
msa363690.2{690_2603}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAATACAA	AGTTTTTTAAT	

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_A909}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAAT
msa363690.2{690_JM9130013}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAAT
msa363690.2{690_H36B}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAAT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	151	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	200
msa363690.2{690_M732}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_M781}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_090}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_CJB110}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_1169NT}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_18RS21}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_2603}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_A909}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_JM9130013}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_H36B}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	201	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	250
msa363690.2{690_M732}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_M781}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_090}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_CJB110}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_1169NT}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_18RS21}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_2603}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_A909}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_JM9130013}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_H36B}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	251	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	300
msa363690.2{690_M732}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_M781}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_090}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_CJB110}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_1169NT}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_18RS21}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_2603}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_A909}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_JM9130013}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_H36B}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	301	GTTCAATATG	ATACAACAAC	TGCACAAGCA	350
msa363690.2{690_M732}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_M781}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_090}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_CJB110}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_1169NT}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_18RS21}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_2603}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_A909}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_JM9130013}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_H36B}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	351	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	400
msa363690.2{690_M732}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_M781}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_090}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_CJB110}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_1169NT}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_18RS21}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_2603}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_A909}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_JM9130013}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_H36B}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	401	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	450
msa363690.2{690_M732}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_M781}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_090}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_CJB110}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_1169NT}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_18RS21}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_2603}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCtTCATC	ATCACAAGGA
msa363690.2{690_A909}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCaTCATC	ATCACAAGGA
msa363690.2{690_JM9130013}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCaTCATC	ATCACAAGGA
msa363690.2{690_H36B}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCaTCATC	ATCACAAGGA
Consensus	***-*****	*****-*	*****	*****-*****	*****
msa363690.2{690_COH1}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_M732}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_M781}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_090}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_CJB110}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_1169NT}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_18RS21}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_2603}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_A909}	CAAGGGgCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_JM9130013}	CAAGGGgCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_H36B}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
Consensus	*****-***	*****	*****	*****	*****
msa363690.2{690_COH1}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_M732}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_M781}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_090}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_CJB110}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_1169NT}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_18RS21}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_2603}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_A909}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_JM9130013}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_H36B}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_M732}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_M781}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_090}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_CJB110}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_1169NT}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_18RS21}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_2603}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_A909}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_JM9130013}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_H36B}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_M732}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_M781}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_090}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_CJB110}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_1169NT}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_18RS21}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_2603}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_A909}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_JM9130013}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_H36B}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_M732}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_M781}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_090}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_CJB110}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_1169NT}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_18RS21}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_2603}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_A909}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_JM9130013}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_H36B}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_M732}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_M781}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_090}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_CJB110}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_1169NT}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_18RS21}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_2603}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_A909}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_JM9130013}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_H36B}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
Consensus	*****-*	*****	*****	*****	*****
msa363690.2{690_COH1}	751	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_M732}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_M781}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_090}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_CJB110}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_1169NT}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_18RS21}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_2603}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_A909}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_JM9130013}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_H36B}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
Consensus	*****-*	*****	*-*****	*****	*****
msa363690.2{690_COH1}	801	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT
msa363690.2{690_M732}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_M781}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_090}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_CJB110}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_1169NT}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_18RS21}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_2603}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_A909}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_JM9130013}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_H36B}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	851	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC
msa363690.2{690_M732}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_M781}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_090}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_CJB110}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_1169NT}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_18RS21}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_2603}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_A909}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_JM9130013}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_H36B}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	901	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA
msa363690.2{690_M732}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_M781}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_090}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_CJB110}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_1169NT}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_18RS21}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_2603}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_A909}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_JM9130013}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_H36B}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	951	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT
msa363690.2{690_M732}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_M781}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_090}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_CJB110}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_1169NT}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_18RS21}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_2603}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_A909}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_JM9130013}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_H36B}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
Consensus	***-*****	*****	*****	*****	*****
msa363690.2{690_COH1}	1001	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG
msa363690.2{690_M732}	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAAT
msa363690.2{690_M781}	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAAT
msa363690.2{690_090}	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAAT
msa363690.2{690_CJB110}	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAAT

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_1169NT}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACITTTGTTTG	GGTATACAAT
msa363690.2{690_18RS21}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTTGTTTG	GGTATACAAT
msa363690.2{690_2603}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTTGTTTG	GGTATACAAT
msa363690.2{690_A909}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTTGTTTG	GGTATACAAT
msa363690.2{690_JM9130013}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTTGTTTG	GGTATACAAT
msa363690.2{690_H36B}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTTGTTTG	GGTATACAAT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_M732}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_M781}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_090}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_CJB110}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_1169NT}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_18RS21}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_2603}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_A909}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_JM9130013}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_H36B}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_M732}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_M781}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_090}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_CJB110}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_1169NT}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_18RS21}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_2603}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_A909}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_JM9130013}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_H36B}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_M732}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_M781}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_090}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_CJB110}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_1169NT}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_18RS21}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_2603}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_A909}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_JM9130013}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_H36B}	TTACTAATCC	AAGtAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
Consensus	*****	***-***-*	*****	*****	*****
msa363690.2{690_COH1}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_M732}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_M781}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_090}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_CJB110}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_1169NT}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_18RS21}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_2603}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_A909}	GAATCAATaG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_JM9130013}	GAATCAATaG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_H36B}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtg-	~
Consensus	*****	*****	*****	*****	---

SEQ ID NO. 8511

STRAIN 2603 frame: 1

MSKRQNLGI SKKGAI ISGLSVALIVVIGGFLWVQS QPNKSAVKTNKYVFNVRREGSVSSST
 LLTGKAKANQEYVYFDANKGNRATVTVKVGDKITAGQQLVQYDTTAAQAYDTANRQLN
 KVARQINNLKTTGSLPAMESSDQSSSSSQGGTQSTSGATNRLQONYQS QANASYNQQLQ
 DLNDAYADAQAEVNKAQKALNDTVITSDVSGTVVEVNSDIDPASKTSQVLVHVATEGKLQ
 VQGTMSYDLANVKKDQAVKIKSKVYPDKWEWEGKISYISNYPEAEANNNDNNSSSAVNY
 KYKVDITSPLDALKQGFVTSVEVNGDKHLIVPTSSVINKDNKHFVWVYNDNNRKRISKVE
 VKIGKADAKTQEILSGLKAGQIVVTNPSKTFKDGQKIDNIESIDLNSNKKSEVK

SEQ ID NO. 8512

STRAIN 090 frame: 1

FLWVQS QPNKSAVKTNKYVFNVRREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTAAQAYDTANRQLN KVARQINNLKTTGSLPAMESSDQSSSSSQ
 GGTTQSTSGATNRLQONYQS QANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDLANVKKDQAVKIKSKVYPDK
 WEWEGKISYISNYPEAEANNNDNNSSSAVNYKYKVDITSPLDALKQGFVTSVEVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNNRKRISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSE

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8513

STRAIN A909 frame: 1

FLWVQSQPNKSAVKNTNYKVFNVREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGAQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVTNKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8514

STRAIN H36B frame: 1

FLWVQSQPNKSAVKNTNYKVFNVREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVTNKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 AFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8515

STRAIN 18RS21 frame: 1

FLWVQSQPNKSAVKNTNYKVFNVREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSE

SEQ ID NO. 8516

STRAIN M732 frame: 1

FLWVQSQPNKSAVKNTNYKVFNVREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8517

STRAIN COH1 frame: 1

FLWVQSQPNKSAVKNTNYKVFNVREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8518

STRAIN M781 frame: 1

FLWVQSQPNKSAVKNTNYKVFNVREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8519

STRAIN M781 frame: 1

FLWVQSQPNKSAVKNTNYKVFNVREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8520

STRAIN CJB110 frame: 1

FLWVQSQPNKSAVKNTNYKVFNVREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8521

Table 85: Comparative Sequences relating to SAG1361

STRAIN 1169NT frame: 1

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FLWVQSQPNKSAVKTNKYVFNREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDITTTAAQAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDLANVKKDQAVKI KSKVYPPDK
EWEGKISYISNYPEAEANNDNSNGSSAVNYKYKVDITSPLDALKQGTFSVEVNVGDKH
LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

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SEQ ID NO. 8522

STRAIN JM9130013 frame: 1

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FLWVQSQPNKSAVKTNKYVFNREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDITTTAAQAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
GQGAQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDLANVKKDQSVKI KSKVYPPDK
EWEGKISYISNYPEAEANNDNSNGSSAVNYKYKVDITSPLDALKQGTFSVEVNVGDKH
LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

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PRETTY of: /biotmp/msa375805.2{*} April 1, 2003 02:58 ..

msa375805.2{690_COH1}	1	50
msa375805.2{690_M732}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_M781}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_090}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_CJB110}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_1169NT}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_18RS21}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_2603}	mskrqnlgis kkgaiisgls valivviggf	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_A909}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_JM9130013}	-----F	LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_H36B}	-----F	LWVQSQPNKS AVKTNKYVFN
Consensus	*****	*****
msa375805.2{690_COH1}	51	100
msa375805.2{690_M732}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_M781}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_090}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_CJB110}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_1169NT}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_18RS21}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_2603}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_A909}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_JM9130013}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
msa375805.2{690_H36B}	VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV	GDKITAGQQL
Consensus	*****	*****
msa375805.2{690_COH1}	101	150
msa375805.2{690_M732}	VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_M781}	VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_090}	VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_CJB110}	VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_1169NT}	VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_18RS21}	VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_2603}	VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_A909}	VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_JM9130013}	VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
msa375805.2{690_H36B}	VQYDITTTAAQ AYDTANRQLN KVARQINNLT TTGSFPAMES	SDQSSSSSQ
Consensus	*****	*****
msa375805.2{690_COH1}	151	200
msa375805.2{690_M732}	QGTQSTSGAT NRLQNNYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_M781}	QGTQSTSGAT NRLQNNYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_090}	QGTQSTSGAT NRLQNNYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_CJB110}	QGTQSTSGAT NRLQNNYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_1169NT}	QGTQSTSGAT NRLQNNYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_18RS21}	QGTQSTSGAT NRLQNNYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_2603}	QGTQSTSGAT NRLQNNYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_A909}	QGTQSTSGAT NRLQNNYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_JM9130013}	QGTQSTSGAT NRLQNNYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
msa375805.2{690_H36B}	QGTQSTSGAT NRLQNNYQSQ ANASYNQQLQ DLNDAYADAQ	AEVNKAQKAL
Consensus	***-*****	*****
msa375805.2{690_COH1}	201	250
msa375805.2{690_M732}	NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ	VQGTMSYIDL
msa375805.2{690_M781}	NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ	VQGTMSYIDL
msa375805.2{690_090}	NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ	VQGTMSYIDL

Table 85: Comparative Sequences relating to SAG1361

msa375805.2{690_CJB110}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_1169NT}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_18RS21}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_2603}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_A909}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_JM9130013}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_H36B}	NDTVITSQVLS	GTVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
Consensus	*****	*****	*****	*****	*****
	251				300
msa375805.2{690_COH1}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_M732}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_M781}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_090}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_CJB110}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_1169NT}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_18RS21}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_2603}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_A909}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_JM9130013}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_H36B}	ANVKKDQaVK	IKSKVYPDK	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
Consensus	*****	*****	*****	*****	*****
	301				350
msa375805.2{690_COH1}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_M732}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_M781}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_090}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_CJB110}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_1169NT}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_18RS21}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_2603}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_A909}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_JM9130013}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_H36B}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
Consensus	*****	*****	*****	*****	*****
	351				400
msa375805.2{690_COH1}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_M732}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_M781}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_090}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_CJB110}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_1169NT}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_18RS21}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_2603}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_A909}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_JM9130013}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_H36B}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
Consensus	*****	*****	*****	*****	*****
	401				414
msa375805.2{690_COH1}	ESIDLKSNKK	SEv-			
msa375805.2{690_M732}	ESIDLKSNKK	SEv-			
msa375805.2{690_M781}	ESIDLKSNKK	SEv-			
msa375805.2{690_090}	ESIDLKSNKK	SEv-			
msa375805.2{690_CJB110}	ESIDLKSNKK	SEv-			
msa375805.2{690_1169NT}	ESIDLKSNKK	SEv-			
msa375805.2{690_18RS21}	ESIDLKSNKK	SEv-			
msa375805.2{690_2603}	ESIDLKSNKK	SEvK			
msa375805.2{690_A909}	ESIDLKSNKK	SEvK			
msa375805.2{690_JM9130013}	ESIDLKSNKK	SEvK			
msa375805.2{690_H36B}	ESIDLKSNKK	SEv-			
Consensus	*****	***			

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8601

STRAIN 2603

atgaaaaaattggaattattgtcctcacactactgacctcttttttggtatcttgcgga
 caacaaactaaacaagaaagcactaaaacaactatttctaaaatgcctaaaattgaaggc
 ttcacctattatggaaaaattcctgaaaatccgaaaaagtaattatttacatatctt
 tacactgggtattttataaaactaggtgttaattgttcaagttacagtttagacttagaa
 aaagatagcccggttttttggttaaacactgaagaagctaaaaaattactgctgatgat
 acagaagctattgcccgcacaaaaacctgatttaatacatggttttcgatcaagatccaaac
 atcaatactctgaaaaaaattgcaccaactttagttatataatattggtgcacaaaattat
 ttagatatgatgccagccttggggaaagtattcggtaaagaaaaagaagctaatacagtg
 gttagccaattggaaaaactaaaactctcgctgtcaaaaaagatttacaccatatcttaag
 cctaacactacttttactattatggatttttatgataaaaatatctatttatatggtaat
 aattttggacgcggtggagaactaatctatgattcactaggttatgctgccccagaaaa
 gtcaaaaaagatgtcttttaaaaaagggtggtttaccgtttcgcaagaagcaatcggtgat
 tacgttggagattatgcccttgttaataataacaaaacgactaaaaagcagcttcatca
 cttaagaaagtgatgtctggaagaatttaccagctgtcaaaaaagggcacatagaa
 agtaactacgagctgttttatttctctgacctctatctttagaagctcaattaaaatca
 tttacaaaggctatcaagaaaaatacaaat

SEQ ID NO. 8602

STRAIN 090

GAAGGCTTCACCTATTATGGAAAAATTCCTGAAAAATCCGAAAAAGTAAT
 TAATTTTACATATTCTTACACTGGGTATTTATTAATACTAGGTGTTAATG
 TTTCAAGTTACAGTTTAGACTTAGAAAAAGATAGCCCCGTTTTTGGTAAAG
 CAACTGAAAGAGCTAAAAAATTAAC'TGCTGATGATACAGAAGCTATTGTC
 CGCACAAAAACCTGATTTAATCATGGTTTTCGATCAAGATCCAAACATCA
 ATACTCTGAAAAAAATTCACCAACTTTAGTTATTAATATGGTGCACAA
 AATTATTTAGATATGATGCCAGCCTTGGGAAAGTATTCGGTAAAGAAAA
 AGAAGCTAATCAGTGGGTTAGCCAATGGAAAACTAAAACTCTCGCTGCCA
 AAAAAAGATTTACCATATCTTAAAGCCTAACACTACTTTTACTATTATG
 GATTTTATGATAAAAAATATCTATTTATATGGTAATAATTTTGGACGCGG
 TGGAGAACTAATCTATGATTCAGTGTATGCTGCCCAgAAAAAGTCA
 AAAAAAGATGTCTTTAAAAAAGGGTGGTTTACCCTTTTCgCAAGAAGCAATC
 GGTGATTACGTTGGAGATTATGCCCTTGTAAATATAACAAAACGACTAA
 AAAAGCAGCTTCatcACTTAAAGAAAGTGATGTCTGGAAGAAATTTACCAG
 CTGTCAAAAAAGGGCACATCATAGAAAGTAacTACGACGTGTTTTATTTC
 TCTGACCTCTATCTTTTAGAAGCTCAATTAAAAATCATTTACAAA

SEQ ID NO. 8603

STRAIN A909

GAAGGCTTCACCTATTATGGAAAAATTCCTG
 AAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGGATATTTA
 TTAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAAAAGA
 TAgCCCCGTTTTTGGTAAaCAACTGAAAGGAGCTAAAAAATTAAC'TGCTG
 ATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAaTCATGGTTTTT
 GATCAAGATCCAAACATCAATACTCTGAAAAAATTCACCAACTTTAGT
 TATTAATATGGTGACAAAAATTTTATagAtaTGATGCCAGCTTTGGGGA
 AAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTAGCCAaTGGAAA
 ACTAAAACTCTCGCTGCCAAAAAAGATTACACCATATCTTAAACCTAA
 CACTACTTTTACCATTATGGATTTTATGATAAAAAATATCTATTTATATG
 GTAATAATTTTGGACGCGGTGGAGAATAATCTATGATTCAGTGTATG
 GCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGTGGTTTAC
 CGTTTCGCAAGAAAGCAATCGGTgATTACGTTGGAGATTATGCCCTTGTTA
 ATATAACAAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAGTGAT
 GTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAAGTAA
 CTACGACGTGTTTTATTCTCTGACCTcTATCTTTAGAAGCTCAATTAA
 AATCATTTACAAA

SEQ ID NO. 8604

STRAIN H36B

GAAGGCTTCACCTATTATGGAAAA
 ATTCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGG
 ATATTTATTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAG
 AAAAAAGATAgCCCCGTTTTTGGTAAgCAACTGAAAGGAGCTAAAAAATTA
 ACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAaTCAT
 GGTTTTTGATCAAgATCCAAACATCAATACTCTGAAAAAATTCACCAAA
 CTTTAGTTATTAAATATGGTGACAAAATTTTATagAtaTGATGCCAGCT
 TTGGGGAaAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTAGCCA
 ATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTACACCATATCTTAA
 GGCTTaACaCTACTTTTACTATTATAGatTTTATGATAAAAAATATCTAT
 TTTATATGGTAATAATTTTGGACGCGGTGGAgAACTAATCTATGATcCACT
 AGGTTATGCTGCCCAgAAAAAGTCAAAAAAgATGTCTTTAAAAAAGGGT
 GGTTTACCCTTTTCgCAAGAAGCAATCGGTgATTACGTTGGAGATTATGCC
 CTTGTTAATATAACAAAACGACTAAAAAAGCAGCTTCaTCACTTAAAGA
 AAGTGATGTTTGGAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAG
 AAAGTAACACGAGCTGTTTTATTCTCTGACCTCTATCTTTAGAAGCT
 CAATTAAATCATTTACAAA

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8605

STRAIN 18RS21

GAAGGCTTCACCTATTATGGA
 AAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
 TGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
 TAGAAAAAGATAGCCCCGTTTTTGGTAACAACACTGAAAGAAGCTAAAAAA
 TTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAAT
 CATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCAC
 CAACCTTAGTTATTAAATATGGTGCACAAAATTATTTAgATaTGATGCCA
 GCCTTGGGGAAAGTATTTCGGTAAGAAAAgAAGCTAATCAGTGGGTTAG
 CCAATGGAAAACTAAAACTCTCGCTGTCAAAAAAGATTACACCATATCT
 TAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATATC
 TATTTATATGGTAATAATTTTGGACGCGGTGGAGAATAATCTATGATTCT
 ACTAGGTTATGCTGCCCCagAAAAAGTCAAAAAgATGTCTTTAAAAAAG
 GGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
 GCCCTTGTTAATATAAAACAAACgACTAAAAAGCAGCTTCATCACTTAA
 AGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACATCA
 TAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAGAA
 GCTCAATTAAATCATTACAAA

SEQ ID NO. 8606

STRAIN M732

GAAGGCTTCACCTATTATGG
 AAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACA
 CTGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
 TTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA
 ATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAA
 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCA
 CCACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATaTGATGCC
 AGCCTTGGGGAAAGTATTTCGGTAAGAAAAAGAGCTAATCAGTGGGTTA
 GCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAGATTACACCATATC
 TTAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATAT
 CTATTTATATGGTAATAATTTTGGACgCGGTGGAGAACTAATCTATGATT
 CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 GGGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTTAATATAAAACAAACGACTAAAAAGCAGCTTCATCACTTA
 AAGAAAGTGATGTCTGGAAGAAATTACCAGCTGTCAAAAAAGGGCACATC
 ATAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAGA
 AGCTCAATTAAATCATTACAAA

SEQ ID NO. 8607

STRAIN COH1

GAAGGCTTCACCTATTATG
 GAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTAC
 ACTGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAgA
 CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAA
 AATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAA
 ATCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGC
 ACCAATTTAGTTATTAAATATGGTGCACAAAATTATTTAgATaTGATGC
 CAGCCTTGGGGAAAGTaTTcGGTAAGAAAAAGAGCTAATCAGTGGGTT
 AGCCAATGGAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATAT
 CTTAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATA
 TCTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGAT
 TCCTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 AGGGTGGTTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 ATGCCCTTGTTAATATAAAACAAACGACTAAAAAGCAGCTTCATCACTT
 AAAGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACAT
 CATAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAG
 AAGCTCAATTAAATCATTACAAA

SEQ ID NO. 8608

STRAIN M781

GAAGGCTTCACCTATTATGG
 AAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACA
 CTGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
 TTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA
 ATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAA
 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCA
 CCACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATaTGATGCC
 AGCCTTGGGGAAAGTATTTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTA
 GCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAGATTACACCATATC
 TTAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATAT
 CTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATT
 CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 GGGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTTAATATAAAACAAACGACTAAAAAGCAGCTTCATCACTTA

Table 86: Comparative Sequences relating to SAG1393

AAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATC
 ATAGAAAGTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAGA
 AGCTCAATTAATAATCATTACAAA

SEQ ID NO. 8609

STRAIN CJB110

GAAGGCTTCACCTATTATGGA

AAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
 TGGGTATTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
 TAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAA
 TTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTAAT
 CATGGTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCAC
 CAACTTAGTTATTAATATGGTGCACAAAATTTATTTAGATATGATGCCA
 GCCTTGGGGAAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTAG
 CCAATGGAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATATCT
 TAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATC
 TATTTATATGTTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTC
 ACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAGATGCTTTAAAAAAG
 GGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
 GCCCTTGTTAATATAACAAAACGACTAAAAAAGCAGCTTCATCACTTAA
 AGAAAGTGATGCTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATCA
 TAGAAAGTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAGAA
 GCTCAATTAATAATCATTACAAA

SEQ ID NO. 8610

STRAIN 1169NT

GAAGGCTTCACCTATTATGGAATAAT

CCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGGGTA
 TTTATTAAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAA
 AAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAATTAAT
 GCTGATGATACAGAAGCTATTGCCGcACAAaaACCTGATTTAATCATGGT
 TTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCACCAACTT
 TAGTTATTAATAATATGGTGCACAAAATTTATTAGATATGATGCCAGCCTTG
 GGGAAAGTATTCGGTAAAGAAAAAGGCTAATCAGTGGGTTAGCCAATG
 GAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATATCTTAAAGC
 CTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATCTATTTA
 TATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTCACCTAGG
 TTATGCTGCCCCAGAAAAAGTCAAAAAGATGCTTTAAAAAAGGGTGGT
 TTACCGTTTTcGCAAGAAGCAATCGGTGATTACGTTGGAGATTATGCCCTT
 GTTAATATAAACAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAG
 TGATGCTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATCATAGAAA
 GTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAGAAGCTCAA
 TTAAATCATTACAAA

SEQ ID NO. 8611

STRAIN JM9130013

GAAGGCTTCACCTATTATG

GAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTAC
 ACTGATATTATTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGA
 CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGGAGCTAAAA
 AATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTA
 ATCATGGTTTTTATCAAGATCCAAACATCAATACTCTGAAAAAATTGTC
 ACCAACTTTAGTTATTAATAATGGTGCACAAAATTTATTTAGATATGATGC
 CAGCTTTGGGGAAGTATTTCGGTAAAGAAAAAGAGCTAATCAGTGGGTT
 AGCCAATGGAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATAT
 CTTAAACCTAACACTACTTTTACCATTATGGATTTTTATGATAAAAATA
 TCTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGAT
 TCACCTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAGATGCTTTAAAAA
 AGGGTGGTTTTACCGTTTTcGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 ATGCCCTTGTTAATATAAACAACGACTAAAAAAGCAGCTTCATCACTT
 AAAGAAAGTGATGCTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACAT
 CATAGAAAGTAACACGACGTGTTTTATTCTCTGACCCCTCTATCTTTAG
 AAGCTCAATTAATAATCATTACAAA

PRETTY of: /biotmp/msa521731.2{*} April 28, 2003 08:07 ..

	1	50
msa521731.2{691_090}	-----	-----
msa521731.2{691_1169NT}	-----	-----
msa521731.2{691_CJB110}	-----	-----
msa521731.2{691_COH1}	-----	-----
msa521731.2{691_M732}	-----	-----
msa521731.2{691_M781}	-----	-----
msa521731.2{691_18RS21}	-----	-----
msa521731.2{691_2603}	atgaaaaaaa	ttggaattat tgtcctcaca ctactgacct tctttttggt

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_A909}	-----	-----	-----	-----	-----
msa521731.2{691_JM9130013}	-----	-----	-----	-----	-----
msa521731.2{691_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa521731.2{691_090}	-----	-----	-----	-----	-----
msa521731.2{691_1169NT}	-----	-----	-----	-----	-----
msa521731.2{691_CJB110}	-----	-----	-----	-----	-----
msa521731.2{691_COH1}	-----	-----	-----	-----	-----
msa521731.2{691_M732}	-----	-----	-----	-----	-----
msa521731.2{691_M781}	-----	-----	-----	-----	-----
msa521731.2{691_18RS21}	-----	-----	-----	-----	-----
msa521731.2{691_2603}	atcttgcgga	caacaaacta	aacaagaaag	cactaaaaca	actatttcta
msa521731.2{691_A909}	-----	-----	-----	-----	-----
msa521731.2{691_JM9130013}	-----	-----	-----	-----	-----
msa521731.2{691_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa521731.2{691_090}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_1169NT}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_CJB110}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_COH1}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_M732}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_M781}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_18RS21}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_2603}	aaatgcctaa	aattGAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_A909}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_JM9130013}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_H36B}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa521731.2{691_090}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_1169NT}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_CJB110}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_COH1}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_M732}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_M781}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_18RS21}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_2603}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_A909}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_JM9130013}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_H36B}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa521731.2{691_090}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_1169NT}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_CJB110}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_COH1}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_M732}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_M781}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_18RS21}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_2603}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_A909}	ACTAGGaGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_JM9130013}	ACTAGGaGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_H36B}	ACTAGGaGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
Consensus	*****	*****	*****	*****	*****
	251				300
msa521731.2{691_090}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_1169NT}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_CJB110}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_COH1}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_M732}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_M781}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_18RS21}	CCGTTTTTGG	TAAaCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_2603}	CCGTTTTTGG	TAAaCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_A909}	CCGTTTTTGG	TAAaCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_JM9130013}	CCGTTTTTGG	TAAgCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_H36B}	CCGTTTTTGG	TAAgCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
Consensus	*****	***-*****	*****	*****	*****
	301				350
msa521731.2{691_090}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_1169NT}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_CJB110}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_COH1}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_M732}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_M781}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_18RS21}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_2603}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_A909}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_JM9130013}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_H36B}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_1169NT}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_CJB110}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_COH1}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_M732}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_M781}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_18RS21}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_2603}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_A909}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_JM9130013}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_H36B}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_1169NT}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_CJB110}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_COH1}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_M732}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_M781}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_18RS21}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_2603}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_A909}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_JM9130013}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_H36B}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_1169NT}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_CJB110}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_COH1}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_M732}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_M781}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_18RS21}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_2603}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_A909}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_JM9130013}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_H36B}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_1169NT}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_CJB110}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_COH1}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_M732}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_M781}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_18RS21}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_2603}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_A909}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_JM9130013}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_H36B}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
Consensus	*****	*-*****	*****	*****	*****
msa521731.2{691_090}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_1169NT}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_CJB110}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_COH1}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_M732}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_M781}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_18RS21}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_2603}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_A909}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_JM9130013}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_H36B}	CTTTTACTAT	TATaGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
Consensus	*****_**	***-*****	*****	*****	*****
	601				650
msa521731.2{691_090}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_1169NT}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_CJB110}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_COH1}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_M732}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_M781}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_18RS21}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_2603}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_A909}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_JM9130013}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_H36B}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
Consensus	*****	*****	*****	*****	*****
	651				700
msa521731.2{691_090}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_1169NT}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_CJB110}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_COH1}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_M732}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_M781}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_18RS21}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_2603}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_A909}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_JM9130013}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_H36B}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
Consensus	*****	*****	*****	*****	*****
	701				750
msa521731.2{691_090}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_1169NT}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_CJB110}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_COH1}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_M732}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_M781}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_18RS21}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_2603}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_A909}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_JM9130013}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_H36B}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
Consensus	*****	*****	*****	*****	*****
	751				800
msa521731.2{691_090}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_1169NT}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_CJB110}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_COH1}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_M732}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_M781}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_18RS21}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_2603}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_A909}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_JM9130013}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_H36B}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
Consensus	*****	*****	*****	*****	*****_**
	801				850
msa521731.2{691_090}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_1169NT}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_CJB110}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_COH1}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_M732}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_M781}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_18RS21}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_2603}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_A909}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_JM9130013}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_H36B}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
Consensus	*****	*****	*****	*****	*****
	851				900
msa521731.2{691_090}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_1169NT}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_CJB110}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_COH1}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_M732}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_M781}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_18RS21}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_2603}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_A909}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_JM9130013}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_H36B}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
Consensus	*****	*****	*****	*****	*****

	901		930
msa521731.2{691_090}	TTTACAAA--	-----	-----
msa521731.2{691_1169NT}	TTTACAAA--	-----	-----
msa521731.2{691_CJB110}	TTTACAAA--	-----	-----
msa521731.2{691_COH1}	TTTACAAA--	-----	-----
msa521731.2{691_M732}	TTTACAAA--	-----	-----
msa521731.2{691_M781}	TTTACAAA--	-----	-----
msa521731.2{691_18RS21}	TTTACAAA--	-----	-----
msa521731.2{691_2603}	TTTACAAA	ctatcaaaga	aaatacaaat
msa521731.2{691_A909}	TTTACAAA--	-----	-----
msa521731.2{691_JM9130013}	TTTACAAA--	-----	-----
msa521731.2{691_H36B}	TTTACAAA--	-----	-----
Consensus	*****	*****	*****

SEQ ID NO. 8612

STRAIN 2603 frame: 1

MKKIGIIVLTLLTFFLVSCGQQTKESTKTTISKMPKIEGFTYYGKIPENPKKVINFTYS
 YTGILLKLGIVNVSSYSLDLEKDSPVFGKQLKEAKKLTADDTEAIAAQKPDLMVFDQDPN
 INTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEANQWVSQWKTTLAVKKDLHHILK
 PNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAPEKVKKDVFKKGWFTVSQEAIGD
 YVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHIIESNYDVFFYFSDPLSLEAQLKS
 FTKAIKENTN

SEQ ID NO. 8613

STRAIN 090 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGILLKLGIVNVSSYSLDLEKDSPVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8614

STRAIN A909 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGILLKLGIVNVSSYSLDLEKDSPVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8615

STRAIN H36B frame: 1

EGFTYYGKIPENPKKVINFTYSYTGILLKLGIVNVSSYSLDLEKDSPVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8616

STRAIN 18RS21 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGILLKLGIVNVSSYSLDLEKDSPVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8617

STRAIN M732 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGILLKLGIVNVSSYSLDLEKDSPVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNNGFRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8618

STRAIN COH1 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGILLKLGIVNVSSYSLDLEKDSPVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN

Table 86: Comparative Sequences relating to SAG1393

QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8619

STRAIN M781 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8620

STRAIN CJB110 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8621

STRAIN 1169NT frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8622

STRAIN JM9130013 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

PRETTY of: /biotmp/msa522124.2{*} April 28, 2003 08:17 ..

	1				50
msa522124.2{691_090}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_1169NT}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_CJB110}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_COH1}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_M732}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_M781}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_18RS21}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_2603}	mkkigiivlt	lltfflvscg	qqtqgestkt	tiskmpkieg	FTYYGKIPEN
msa522124.2{691_A909}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_JM9130013}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_H36B}	-----	-----	-----	-----	EG FTYYGKIPEN
Consensus	*****	*****	*****	*****	*****
	51				100
msa522124.2{691_090}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_1169NT}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_CJB110}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_COH1}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_M732}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_M781}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_18RS21}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_2603}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_A909}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KgAKKLtADD
msa522124.2{691_JM9130013}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KgAKKLtADD
msa522124.2{691_H36B}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KgAKKLtADD
Consensus	*****	*****	*****	*****	*-*****
	101				150
msa522124.2{691_090}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_1169NT}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_CJB110}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_COH1}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_M732}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_M781}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_18RS21}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_2603}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_A909}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_JM9130013}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV

Table 86: Comparative Sequences relating to SAG1393

msa522124.2{691_H36B}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
Consensus	*****	*****	*****	*****	*****
	151				200
msa522124.2{691_090}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_1169NT}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_CJB110}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_COH1}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_M732}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_M781}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_18RS21}	FGKEKEANQW	VSQWKTKTTLA	vKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_2603}	FGKEKEANQW	VSQWKTKTTLA	vKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_A909}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_JM9130013}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_H36B}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
Consensus	*****	*****	*****	*****	*****
	201				250
msa522124.2{691_090}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_1169NT}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_CJB110}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_COH1}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_M732}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_M781}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_18RS21}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_2603}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_A909}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_JM9130013}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_H36B}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
Consensus	*****	*****	*****	*****	*****
	251				300
msa522124.2{691_090}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_1169NT}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_CJB110}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_COH1}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_M732}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_M781}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_18RS21}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_2603}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_A909}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_JM9130013}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
msa522124.2{691_H36B}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVFFYFSD	PLSLEAQLKS
Consensus	*****	*****	*****	*****	*****
	301	310			
msa522124.2{691_090}	FT-----				
msa522124.2{691_1169NT}	FT-----				
msa522124.2{691_CJB110}	FT-----				
msa522124.2{691_COH1}	FT-----				
msa522124.2{691_M732}	FT-----				
msa522124.2{691_M781}	FT-----				
msa522124.2{691_18RS21}	FT-----				
msa522124.2{691_2603}	FTkaikentn				
msa522124.2{691_A909}	FT-----				
msa522124.2{691_JM9130013}	FT-----				
msa522124.2{691_H36B}	FT-----				
Consensus	*****				

Table 87: Comparative Sequences relating to SAG0645

SEQ ID NO. 8701

STRAIN 2603

ATGAAATATCGAAGAAGTTATTGTTTTCGGCTGCTGTT
 TTAACAATGGTGGCGGGTCAACTGTTGAACCAAGTAGCTCAGTTTGGCGACTGGAATGAGT
 ATTGTAAGAGCTGCAGAAGTGTCAAGAAGCGCCAGCGAAAAACAACAGTAAATATCTAT
 AAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAATGGTGGTATCGAGAATAAA
 GACGGCGAAGTAATATCTAACTATGCTAACTTGGTGACAATGTAAAAGGTTTGCAAGGT
 GTACAGTTTAAACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTG
 ACAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAGTCTA
 CCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGATTCAAAAAAGTAATGTG
 AGATACTTGTATGTAGAAGATTTAAAGAATTACCTTCAAACATTACCAAAGCTTATGCT
 GTACCGTTTGTGTTGGAATTACCAGTTGCTAACTCTACAGGTACAGGTTTCCCTTCTGAA
 ATTAATATTTACCTTAAAAACGTTGTAACCTGATGAACCAAAACAGATAAAGATGTTAAA
 AAATTAGGTGAGGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTTGAAA
 TCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTGAAATTAAGTATAAATTTGCA
 GATGGCTTGACTTATAAATCTGTTGGAATAAATCAAGATTGGTTGAAAAACACTGAATAGA
 GATGAGCACTACACTATTGATGAACCAACAGTTGATAACCAAAATACATTAATAATTACG
 TTTAAACAGAGAAATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCTTGTGTTAAA
 AATCAAGATGCTCTTGTATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAAATT
 CCAAGTTGCTCAACTATTAATGAAAAAGCAGTTTAGGAAAGCAATTGAAAAATCTTTT
 GAAGTTCAATATGACATACTCTCTGATAAAGCTGACAAATCCAAACCACTAATCCTCCA
 AGAAACAGAGAGTTTCACTGTTGGGAAACGATTGTAAGAAAGACTCAACAGAAACA
 CAAACACTAGGTGGTCTGAGTTTGAATTTGTTGGCTTCTGATGGGACAGCAGTAAATGG
 ACAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATGCTGGAGAAGCTGTTACT
 GGGCAACCAATCAAAATTGAAATCAGATACAGACGGTACGTTTGAAGTTAAAGGTTTGGCT
 TATGCAAGTTGATGCGAATGCAAGGGTACAGCAGTAACCTTACAATTTAAAGAAACAAAA
 GCACCAGAAGGTTATGTAATCCCTGATAAAGAAATCGAGTTTACAGTATCAGAAACATCT
 TATAATACAAACCACTGACATCAGGTTGATAGTCTGATGCAACCTGATACAAATT
 AAAAAACAAACCACTGCTTCAATCCCTAATACTGGTGGTATGTTACGGCTATCTTTGTC
 GCTATCGGTGCTGCGGTGATGGCTTTTGTGTTAAGGGATGAAGCGTCTACAAAGAT
 AAC

SEQ ID NO. 8702

STRAIN 090

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGA
 TTTCAAAAAGTAAATGTGAGTACTTGTATGTAGAAGATTAAAGAATTAC
 CTTCAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTTACCC
 TAAAAACGTTGTAACCTGATGAACCAAAACAGATAAAGATGTTAAAAAAT
 TAGGTGAGACGATGCAAGTTTATACGATTGGTGAAGAATTCAAATGGTTCT
 TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCA
 AGATTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAATAAATACGTTTAAACAGAGAA
 ATTTAAAGAAATGCTGAGCTACTTAAAGGAATGACCTTGTGTTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAATAACAGATGATGCGGCATTTTGG
 GAAATTCAGTTGCACTCACTATTAAATGAAAAAGCAGTTTGGGAAAAAGC
 AATTGAAAAATCTTTTGAACCTTCAATATGACCATACCTGATAAAGCTG
 ACAATCCAAACCATCTAACTCTCAAGAAACCAAGAGTTTCACTAGGT
 GGGAAACGATTGTAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
 TGCTGAGTTTGAATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAGCGAATACTAATAAAAACTATATGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATGAAATCACATACAGACGGTACGTTTGA
 GATTAAAGGTTTGGCTTATGCAAGTTGATGCGAATGCAAGGGTACAGCAG
 TAACTTACAAATTAAGAAACAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCAGAAACATCTTATAATACAAACCC
 AACTGACATCAGGTTGATAGTGCTGATGCAACCTGATACAAATTAATA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8703

STRAIN A909

GCAGAAGTGTCAAGAAGCGCCAGCGAA
 AACCAACAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAA
 TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
 TATGCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAA
 ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
 CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
 GTCAAGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCT
 GGAATCAAAAAGTAAATGTGAGTACTTGTATGTAGAAGATTAAAGAATT
 CACCTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
 CCAGTTGCTAACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTTA
 CCCTAAaAACGTTGTAACCTGATGAACCAAAACAGATAAAGATGTTAAAA
 AATTAGGTGAGGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGG
 TTCTTGAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTGGA
 AATTACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAA
 TCAAGATTGGTTGAAAAACCTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAATAATTACGTTTAAACCGA

Table 87: Comparative Sequences relating to SAG0645

GAAATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCCTTGTAAAA
 ATCAAGATGCTCTTGATAAAGCTACTGCAATACAGATGATGCGGCATTT
 TTGGAAATTCAGTTGTCATCAACTATTAATGAAAAAGCAGTTTATAGGAAA
 AGCAATTGAAAACTCTTTGAACTTCAATATGACCATACTCCTGATAAAG
 CTGACAAATCCAAAACCATCTAATCCTCCAGAAAACCCAGAAGTTCATACT
 GGTGGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGG
 TGGTGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGGA
 CAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
 GCTGTACTGGGCAACCAATCAAATGAAATCACAATACAGACGGTACGTT
 TGAGATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAG
 CAGTAACCTTACAAATTAAAAAGAAAACAAAGCACCAGAAGGTTATGTAATC
 CCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAA
 ACCAACTGACATCACGGTTGATAGTCTGATGCAACACCTGATACAAATTA
 AAAACAACAA

SEQ ID NO. 8704

STRAIN 18RS21

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAAC
 AGCATAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAAACGATTCCTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
 TTCAAAAGTAATGTGAGATACTTGTATGTAGAAGATTAAAGAATTACAC
 CTTCAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCCCTTCTGAAATTAATATTTACCC
 TAAAAACGTTGTAACCTGATGAACCAAAAAAGATGTTAAATAAT
 TAGGTACGAGCAGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAAATCTACAATCCCTGCCAATTAGGTGACATGAAAAAATTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAATCA
 AGATTGGTTTCGAAAACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCACAGTTGATAACCAAAATACATTAAAAAATTACGTTTAAACCAAGAGAA
 ATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGT
 GAAATTCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTATAGGAAAAGC
 AATTGAAAAATCTTTTGAACCTCAATATGACCACTACTCCTGATCAAGCTG
 ACAATCCAAACCATCTAATCCTCCAGAAAACCCAGAAGTTCATACCTGGT
 GGGAAACGATTTGTAAAGAAAGACTCAACAGAAAACACAAACCTAGGTGG
 TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATTTGAAATCACAATACAGACGGTACGTTTGA
 GATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG
 TAACCTACAAATTTAAAGAAACAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAACCC
 AACTGACATCACGGTTGATAGTCTGATGCAACACCTGATACAAATTAATA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8705

STRAIN M732

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAACAGT
 AAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTAATCTTA
 ATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAA
 CTTGGTGACAATGTAAAGGTTTGCAAGGTGTACAGTTTAAACGTTATAA
 AGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGTGT
 AAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAGTCTA
 CCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATTCAAA
 AAGTAATGTGAGATACTTGTATGTAGAAGATTAAAGAATTACCTTCAA
 ACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGTTGCT
 AACTCTACAGGTACAGGTTTCTTCTGAAATTAATATTACCCTAAAAA
 CGTTGTAACTGATGAACCAAAAAACAGATAAAGATGTTAAAAAATTAGGTC
 AGGACGATGCAAGTTATACGATTTGGTGAAGAATTCAAATGGTTCTTGAAA
 TCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAATTACTGA
 TAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAAATCAAGATTG
 GTTCGAAAACTGAATAGAGATGAGCACTACACTATTGATGAACCAACA
 GTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAAGAGAAATTAA
 AGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATCAAGATG
 CTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGGAAATT
 CCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTATAGGAAAAGCAATTGA
 AAATACTTTTGAACCTCAATATGACCATACTCCTGATAAAGCTGACAATC
 CAAAAACATCTAATCCTCCAGAAAACCCAGAAGTTCATACTGGTGGGAAA
 CGATTGTAAAGAAAGACTCAACAGAAAACACAAACACTAGGTGGTGTGA
 GTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTC
 TTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACT
 GGGCAACCAATCAAATTTGAAATCACAATACAGACGGTACGTTTGAATTA
 AGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAGCAGTAACCT
 ACAATTTAAAGAAACAAAGCACCAGAAGGTTATGTAATCCCTGATAAA
 GAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAACCAACTGA
 CATCACGGTTGATAGTCTGATGCAACACCTGATACAAATTAATAAACAACA
 AACGTCCTTCA

SEQ ID NO. 8706

STRAIN COH1

Table 87: Comparative Sequences relating to SAG0645

GCAGAAGTGTCAACAAGACGCCAGCGAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTTnTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
 TTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCAC
 CTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTACCC
 TAAAAACGTTGTAACGTGATGAACCAAAACAGATAAAGATGTTAAAAAAT
 TAGGTGAGGACGATGACAGTTTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCA
 AGATTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAGAA
 ATTTAAAGAAATGTCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAATACAGATGATGCGGCATTTTGTG
 GAAATTCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTTAGGAAAAAGC
 AATTGAAAAATACTTTGAACCTCAATATGACCATACTCCTGATAAAGCTG
 ACAATCCAAACCAATCTAATCCTCCAAGAAACAGAAAGTTCACTAGGT
 GGGAAACGATTTGTAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
 TGTGAGTTTGTGATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATAAAGCGAATACTAATAAAAACTATATTGCTGGAGAGCT
 GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
 GATTAAGGTTTGGCTTATGCAAGTTGATGCGAATGACAGGGGTACAGCAG
 TAACTTCAAAATTAAGAAACAAAGCACCAGAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCAAAACATCTTATAATACAAACCC
 AACTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTAATA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8707

STRAIN M781

GCAGAAGTGTCAACAAGACGCCAGCGAAAACAG
 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC
 TAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAAACGTT
 ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACA
 GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAG
 TCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATT
 CAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTACCT
 TCAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGT
 TGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTACCTTA
 AAAACGTTGTAACTGATGAACCAAAACAGATAAAGATGTTAAAAAATTA
 GGTGAGGACGATGACAGTTTATACGATTGGTGAAGAATTCAAATGGTTCTT
 GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTGAAATTA
 CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCAAG
 ATTTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACC
 AACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAGAAAT
 TTAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATCAA
 GATGCTCTTGATAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGTA
 AATTCCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTTAGGAAAAAGCAA
 TTGAAAAATCTTTTGAACCTTCAATATGACCATACTCCTGATAAAGCTGAC
 AATCCAAACCAATCTAATCCTCCAAGAAACAGAAAGTTCACTAGGTGG
 GAAACGATTTGTAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTG
 CTGAGTTTGTGATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGAT
 GCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT
 TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAAGA
 TTAAGGTTTGGCTTATGCAAGTTGATGCGAATGACAGGGGTACAGCAGTA
 ACTTACAAATTAAGAAACAAAGCACCAGAAAGTTATGTAATCCCTGA
 TAAAGAAATCGAGTTTACAGTATCAAAACATCTTATAATACAAACCAA
 CTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTAATAAC
 AACAAACGT

SEQ ID NO. 8708

STRAIN CJB110

GCAGAAGTGTCAACAAGACGCCAGCGAA
 AACAGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATGGAAA
 TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
 TATGCTAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAA
 ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
 CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
 GTGAGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCT
 GGATTCAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATT
 CACCTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
 CCAAGTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATT
 CCTTAAAAACGTTGTAATGATGAACCAAAACAGATAAAGATGTTAAAA
 AATTAGGTGAGGACGATGACAGTTTATACGATTGGTGAAGAATTCAAATGG
 TTCTTGAAGTCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGA
 AATTACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAA
 TCAAGATTGGTTGAAAAACACTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAA
 GAAATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAA

Table 87: Comparative Sequences relating to SAG0645

ATCAAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTT
 TTGGAAATTCAGTTGTCATCAACTATTAATGAAAAAGCAGTTTATAGGAAA
 AGCAATTGAAAACTCTTTGAACTTCAATATGACCATACTCCTGATAAAG
 CTGCAATcCAAAACCATCTAATCCTCCAGAAAACAGAGTTTCATACT
 GGTGGGAAACGATTTGTAAAGAAAGACTCAACAGAAAACAAACACTAGG
 TGGTGCTGAGTTTGATTGTTGGCTTCTGATGGGACAGCAGTAAATGGA
 CAGATGCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
 GCTGTTACTGGGCAACCAATCAAAATGAAATCACATACAGACGGTACGTT
 TGAGATTAAAGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAG
 CAGTAACCTACAAATTAAAGAAAACAAAGCACCAGAGGTTATGTAATC
 CCTGATAAAGAAATCGAGTTTACAGTATCACAACATCTTATAATCCAAA
 ACCAATGACATCAGGTTGATAGTGCTGATGCAACCTGTATACAATTA
 AAAACAACAAACGCTCCTCA

SEQ ID NO. 8709

STRAIN JM9130013

GCAGAAGTGTCAAGAACGCCAGCGAAAACAGCAGTA
 AATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAA
 TGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAAC
 TTGGTGACAAATGTAAGAGGTTTGAAGGTGATCAGTTTAAACGTTATAAA
 GTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGTTGA
 AGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAGTCTAC
 CTCAAAAAATAATGCTCAAGGTTTGGTCTGTCGATGCTCTGGATTCAAAA
 AGTAATGTGAGATACCTGTATGTAGAAGATTTAAAGAATTACCTTCAAA
 CATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGTTGCTA
 ACTCTACAGGTACAGGTTTCCCTTCTGAAATTAATATTACCTAAAAAC
 GTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAAAAATTAGGTCA
 GGACGATGCAAGTTATACGATTGGTGAAGAATTCAAAATGGTTCTTGAAAT
 CTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAATTACTGAT
 AAATTTGAGATGGCTTGACTTATAAATCTGTTGGAATAATCAAGATTGG
 TTCGAAAAACCTGAATAGAGATGAGCACTACACTATTGATGAACCAACAG
 TTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAGAAATTTAAA
 GAAATTTGCTGAGCTACTTAAAGGAATGACCTTGTATAAAATCAAGATGC
 TCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAAATTC
 CAGTTGCTCAACTATTAAATGAAAAAGCAGTTTATAGGAAAAGCAATTGAA
 AATACTTTTGAACCTCAATATGACCATACTCTGATAAAGCTGACAAATCC
 AAAACCACTAATcCTcCAAGAAAACAGAAAGTTCATCTGGTGGGAAAC
 GATTGTGTAAGAAAGACTCAACAGAAAACAAACACTAGGTGGTGTCTGAG
 TTTGATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTCT
 TATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACTG
 GGCACCAATCAAATTGAAATCACATACAGACGGTACGTTTGGATTAAAG
 GGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAGCAGTAACCTA
 CAAATTAAGAAAACAAAGCACCAGAGGTTATGTAATCCCTGATAAAG
 AAATCGAGTTTACAGTATCACAACATCTTATAATAACAAACCACTGAC
 ATCAGGTTGATAGTGCTGATGCAACACCTGATACAATTAACAAACAAAC
 ACGTCTCTCA

PRETTY of: /biotmp/msa123961.2{*} April 30, 2003 07:17 ..

	1				50
msa123961.2{80_2603}	atgaaattat	cgaagaagtt	attgtttttcg	gctgctgttt	taacaatggt
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----

	51				100
msa123961.2{80_2603}	ggcgggggtca	actgttgaac	cagtagctca	gtttgcgact	ggaatgagta
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----

	101				150
msa123961.2{80_2603}	ttgtaagagc	tGCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_A909}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_M732}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_090}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_COH1}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_M781}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{801_JM9130013}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_18RS21}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80h_CJB110}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAgCAGTA
Consensus	-----	*****	*****	*****	*****
msa123961.2{80_2603}	151	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80_A909}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80_M732}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80_090}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80_COH1}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80_M781}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{801_JM9130013}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80_18RS21}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80h_CJB110}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
Consensus		*****	*****	*****	*****
msa123961.2{80_2603}	201	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80_A909}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80_M732}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80_090}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80_COH1}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80_M781}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{801_JM9130013}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80_18RS21}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80h_CJB110}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
Consensus		*****	*****	*****	*****
msa123961.2{80_2603}	251	TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80_A909}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80_M732}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80_090}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80_COH1}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80_M781}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{801_JM9130013}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80_18RS21}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80h_CJB110}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
Consensus		*****	*****	*****	*****
msa123961.2{80_2603}	301	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80_A909}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80_M732}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80_090}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80_COH1}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80_M781}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{801_JM9130013}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80_18RS21}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80h_CJB110}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
Consensus		*****	*****	*****	*****
msa123961.2{80_2603}	351	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80_A909}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80_M732}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80_090}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80_COH1}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80_M781}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{801_JM9130013}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80_18RS21}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80h_CJB110}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
Consensus		*****	*****	*****	*****
msa123961.2{80_2603}	401	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80_A909}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80_M732}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80_090}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80_COH1}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80_M781}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{801_JM9130013}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80_18RS21}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80h_CJB110}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
Consensus		*****	*****	*****	*****
msa123961.2{80_2603}	451	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT
msa123961.2{80_A909}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT
msa123961.2{80_M732}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT
msa123961.2{80_090}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT
msa123961.2{80_COH1}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT
msa123961.2{80_M781}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT
msa123961.2{801_JM9130013}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_18RS21}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80h_CJB110}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_A909}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_M732}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_090}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_COH1}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_M781}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{801_JM9130013}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_18RS21}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80h_CJB110}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_A909}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_M732}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_090}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_COH1}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_M781}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{801_JM9130013}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_18RS21}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80h_CJB110}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80_A909}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80_M732}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80_090}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80_COH1}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80_M781}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{801_JM9130013}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80_18RS21}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80h_CJB110}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_A909}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_M732}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_090}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_COH1}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_M781}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{801_JM9130013}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_18RS21}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80h_CJB110}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_A909}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_M732}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_090}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_COH1}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_M781}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{801_JM9130013}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_18RS21}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80h_CJB110}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_A909}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_M732}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_090}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_COH1}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_M781}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{801_JM9130013}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_18RS21}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80h_CJB110}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTTGAT	GAACCAACAG
msa123961.2{80_A909}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTTGAT	GAACCAACAG
msa123961.2{80_M732}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTTGAT	GAACCAACAG
msa123961.2{80_090}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTTGAT	GAACCAACAG
msa123961.2{80_COH1}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTTGAT	GAACCAACAG
msa123961.2{80_M781}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTTGAT	GAACCAACAG

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{801_JM9130013}	TTGAAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_18RS21}	TTGAAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80h_CJB110}	TTGAAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
Consensus	*****	*****	*****	*****	*****
	851				900
msa123961.2{80_2603}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_A909}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_M732}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_090}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_COH1}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_M781}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{801_JM9130013}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_18RS21}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80h_CJB110}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
Consensus	*****	*****	*****	*****	*****
	901				950
msa123961.2{80_2603}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80_A909}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80_M732}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80_090}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80_COH1}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80_M781}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{801_JM9130013}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80_18RS21}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
msa123961.2{80h_CJB110}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC
Consensus	*****	*****	*****	*****	*****
	951				1000
msa123961.2{80_2603}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_A909}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_M732}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_090}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_COH1}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_M781}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{801_JM9130013}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_18RS21}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80h_CJB110}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa123961.2{80_2603}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_A909}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_M732}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_090}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_COH1}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_M781}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{801_JM9130013}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_18RS21}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80h_CJB110}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa123961.2{80_2603}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_A909}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_M732}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_090}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_COH1}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_M781}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{801_JM9130013}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_18RS21}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80h_CJB110}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa123961.2{80_2603}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_A909}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_M732}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_090}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_COH1}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_M781}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{801_JM9130013}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_18RS21}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80h_CJB110}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
Consensus	*****	*****	*****	*****	*****
	1151				1200
msa123961.2{80_2603}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_A909}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_M732}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_090}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_COH1}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_M781}	GATTGTGAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCCTGAG
msa123961.2{801_JM9130013}	GATTGTGAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCCTGAG
msa123961.2{80_18RS21}	GATTGTGAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCCTGAG
msa123961.2{80h_CJB110}	GATTGTGAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCCTGAG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_A909}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_M732}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_090}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_COH1}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_M781}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{801_JM9130013}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_18RS21}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80h_CJB110}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_A909}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_M732}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_090}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_COH1}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_M781}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{801_JM9130013}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_18RS21}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80h_CJB110}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_A909}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_M732}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_090}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_COH1}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_M781}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{801_JM9130013}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_18RS21}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80h_CJB110}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_A909}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_M732}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_090}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_COH1}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_M781}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{801_JM9130013}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_18RS21}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80h_CJB110}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_A909}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_M732}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_090}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_COH1}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_M781}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{801_JM9130013}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_18RS21}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80h_CJB110}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	AAATCGAGTT	TACAGTATCA	CAAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_A909}	AAATCGAGTT	TACAGTATCA	CAAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_M732}	AAATCGAGTT	TACAGTATCA	CAAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_090}	AAATCGAGTT	TACAGTATCA	CAAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_COH1}	AAATCGAGTT	TACAGTATCA	CAAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_M781}	AAATCGAGTT	TACAGTATCA	CAAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{801_JM9130013}	AAATCGAGTT	TACAGTATCA	CAAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_18RS21}	AAATCGAGTT	TACAGTATCA	CAAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80h_CJB110}	AAATCGAGTT	TACAGTATCA	CAAAACATCTT	ATAATaCAAA	ACCAACTGAC
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_A909}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_M732}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_090}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_COH1}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_M781}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{801_JM9130013}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_18RS21}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80h_CJB110}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	acgtccttca	atccctaata	ctgggtggtat	tggtacggct	atctttgtcg
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_090}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_COH1}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_M781}	acgt-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_18RS21}	acgtccttca	-----	-----	-----	-----
msa123961.2{80h_CJB110}	acgtccttca	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----
msa123961.2{80_2603}	ctatcgggtgc	tgccggtgatg	gctttttgctg	ttaaggggat	gaagcgtcgt
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----
msa123961.2{80_2603}	acaaaagata	ac			
msa123961.2{80_A909}	-----	--			
msa123961.2{80_M732}	-----	--			
msa123961.2{80_090}	-----	--			
msa123961.2{80_COH1}	-----	--			
msa123961.2{80_M781}	-----	--			
msa123961.2{801_JM9130013}	-----	--			
msa123961.2{80_18RS21}	-----	--			
msa123961.2{80h_CJB110}	-----	--			
Consensus	-----	--			

SEQ ID NO. 8710

STRAIN 2603 frame: 1

MKLKKLLFSAAVLTVMAGSTVEPVAQFATGMSIVRAAEVSQERPAKTTVNIYKLQADSY
 KSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFKRYKVKTIDISVDELKKLTVEAAD
 AKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLYVEDLKNSPSNITKAYAVPFVLEL
 PVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQDDAGYTI GEEFKWFLKSTIPANL
 GDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNONTLKITFKPEKFK
 EIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVASTINEKAVLGKAIENTFELQYDHT
 PDKADNPSPNPPRKPEVHTGGKRFVKKDSTETQTLGGAEFDLLASDGTAVKWTDALIKA
 NTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVDANAEGTAVTYKLKETKAPEGYVI
 PDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNKRPSIPTGTGIGTAIFVAIGAAMV
 AFVAVKGMKRRTKDN

SEQ ID NO. 8711

STRAIN 090 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTIDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLEL PVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNONTLKITFKPEKFK EIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPSPNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8712

STRAIN 18RS21 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTIDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLEL PVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNONTLKITFKPEKFK EIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPSPNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8713

STRAIN M732 frame: 1

AEVSQERPAKTTVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK

Table 87: Comparative Sequences relating to SAG0645

RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAGGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKNPPRKPVEHTGGKRFVKKDSSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8714

STRAIN M781 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAGGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKNPPRKPVEHTGGKRFVKKDSSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
R

SEQ ID NO. 8715

STRAIN COH1 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAGGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKNPPRKPVEHTGGKRFVKKDSSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8716

STRAIN CJB110 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAGGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKNPPRKPVEHTGGKRFVKKDSSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8717

STRAIN JM9130013 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAGGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKNPPRKPVEHTGGKRFVKKDSSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8718

STRAIN A909 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAGGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKNPPRKPVEHTGGKRFVKKDSSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK

PRETTY of: /biotmp/msa124060.2{*} April 30, 2003 07:19 ..

	1		50
msa124060.2{80_2603}	mklskklfs	aavltmvags	tvepvafat gmsivraAEV SQERPAKtTv
msa124060.2{80_M732}	-----	-----	-----AEV SQERPAKtTv
msa124060.2{80_A909}	-----	-----	-----AEV SQERPAKtTv
msa124060.2{80_090}	-----	-----	-----AEV SQERPAKtTv
msa124060.2{80_M781}	-----	-----	-----AEV SQERPAKtTv
msa124060.2{80_COH1}	-----	-----	-----AEV SQERPAKtTv
msa124060.2{801_JM9130013}	-----	-----	-----AEV SQERPAKtTv
msa124060.2{80_18RS21}	-----	-----	-----AEV SQERPAKtTv
msa124060.2{80h_CJB110}	-----	-----	-----AEV SQERPAKtTv
Consensus	-----	-----	-----*** *****

Table 87: Comparative Sequences relating to SAG0645

	51		100
msa124060.2{80_2603}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_M732}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_A909}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_090}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_M781}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_COH1}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{801_JM9130013}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_18RS21}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80h_CJB110}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
Consensus	***** _-***-***** ***** ***** *****		
	101		150
msa124060.2{80_2603}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_M732}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_A909}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_090}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_M781}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_COH1}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{801_JM9130013}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_18RS21}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80h_CJB110}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
Consensus	***** ***** ***** ***** *****		
	151		200
msa124060.2{80_2603}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_M732}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_A909}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_090}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_M781}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_COH1}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{801_JM9130013}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_18RS21}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80h_CJB110}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
Consensus	***** ***** ***** ***** *****		
	201		250
msa124060.2{80_2603}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_M732}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_A909}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_090}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_M781}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_COH1}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{801_JM9130013}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_18RS21}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80h_CJB110}	VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
Consensus	***** _-***-***** ***** ***** *****		
	251		300
msa124060.2{80_2603}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_M732}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_A909}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_090}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_M781}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_COH1}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{801_JM9130013}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_18RS21}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80h_CJB110}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
Consensus	***** ***** ***** ***** *****		
	301		350
msa124060.2{80_2603}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_M732}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_A909}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_090}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_M781}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_COH1}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{801_JM9130013}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_18RS21}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80h_CJB110}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
Consensus	***** ***** ***** ***** *****		
	351		400
msa124060.2{80_2603}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80_M732}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80_A909}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80_090}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80_M781}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80_COH1}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{801_JM9130013}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80_18RS21}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
msa124060.2{80h_CJB110}	NTFELQYDHT PDKADNP KPS NPPRKPEVHT GGRFVKKDS TETQTLGGAE		
Consensus	***** ***** ***** ***** *****		

Table 87: Comparative Sequences relating to SAG0645

	401			450
msa124060.2{80_2603}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_M732}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_A909}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_090}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_M781}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_COH1}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{801_JM9130013}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_18RS21}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80h_CJB110}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
Consensus	*****	*****	*****	*****
	451			500
msa124060.2{80_2603}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_M732}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_A909}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_090}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_M781}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_COH1}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{801_JM9130013}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_18RS21}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80h_CJB110}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNpKPTD
Consensus	*****	*****	*****	*****
	501			550
msa124060.2{80_2603}	ITVDSADATP	DTIKNNkrps	ipntggigta	ifvaigaavm afavkgmkrr
msa124060.2{80_M732}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{80_A909}	ITVDSADATP	DTIKNN----	-----	-----
msa124060.2{80_090}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{80_M781}	ITVDSADATP	DTIKNNkr--	-----	-----
msa124060.2{80_COH1}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{801_JM9130013}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{80_18RS21}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{80h_CJB110}	ITVDSADATP	DTIKNNkrps	-----	-----
Consensus	*****	*****	-----	-----
	551			
msa124060.2{80_2603}	tkdn			
msa124060.2{80_M732}	----			
msa124060.2{80_A909}	----			
msa124060.2{80_090}	----			
msa124060.2{80_M781}	----			
msa124060.2{80_COH1}	----			
msa124060.2{801_JM9130013}	----			
msa124060.2{80_18RS21}	----			
msa124060.2{80h_CJB110}	----			
Consensus	----			

Table 88: Comparative Sequences relating to SAG0477

SEQ ID NO. 8801

STRAIN 2603

ATGCCCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATTGTCTTAACGGAATGGCAA
 AAGCGTAACCTTGAATTTTAAAAAACGCAAGAGATGAAGAAGAACAAAAACGTATT
 AACGAAAAATTACGCTTAGATAAAAAGTAATTAATATTCTTCTCCTGAAGAACCT
 CAAATACCTACTAAAATTAAGAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAACTAATCGCATTAGAACT
 GCACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTCCGTTTTCCTACTAATCCT
 TTTAGTAAGCAAAAAACAAATACAGTTAGTGGAAATCAGCATACCTGATGATATTTTG
 ATAGAGAAAAACGAAATATTCAAAAAACGATTAATTTCTTTCTTTAATTTTAAACATAAA
 GCTATTGAACAACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATGTCATATGCACAT
 ACAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAGGCTGATCCTGTAAATAGT
 TCAGAGCTACCAAGCACTTCTTAACAATTAACCTTGATAAGGAAGATAGTATTAAAGCTA
 TTAATTAAAGATTAAAGGCTTTAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGT
 TTAGCTGATTCTAAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGT
 ATTAGAATACCAATTCTTAAATTTAAAGAAAGACTTCTCTTTTACAAACAAATTAAGAAG
 AACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAAACAAATACC
 ATTGAATCAACCCCTGTAAAGCAGAAGATACAAAAATAAATCAACTGATAAAACACAA
 ACACAAATGGTCAGGTTGCGGAAATAGTCAAGGACAAACAAATAACTCAAACTAAT
 CAACAAGGACACAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8802

STRAIN H36B

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAGACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAACTAATCGCA
 TTAGAAGCTGACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTTCC
 GTTTTCTCTACTAATCCTTTTAGTAAGCAAAAAACAAATACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTGTAGAGAAAAACGAATATTCAAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAG
 GCTGATCCTGTAAATAGTTTCAAGCTACCAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCTCTTTTACAAACAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACCAACAAATACCATTTGAATCAACCCCTGTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAAACACAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATAACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8803

STRAIN 18RS21

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAGACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAACTAATCGCA
 TTAGAAGCTGACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTTCC
 GTTTTCTCTACTAATCCTTTTAGTAAGCAAAAAACAAATACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTGTAGAGAAAAACGAATATTCAAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAG
 GCTGATCCTGTAAATAGTTTCAAGCTACCAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCTCTTTTACAAACAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACCAACAAATACCATTTGAATCAACCCCTGTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAAACACAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATAACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8804

STRAIN M732

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAG
 TTGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAAAATTAAAGAGCTTCATTTTCCAAAGATTTCAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAACTAATCG
 CATTAGAAGCTGACCTATATTGTAGTAGCATTCCTAGTCATTTAGTTT

Table 88: Comparative Sequences relating to SAG0477

CCGTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC
 ATATGCACATACAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAA
 AGGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATT
 CTAAAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACA
 AATTAAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAAAAATAAATCAACTGATAAAACACAACACAAAATGGTCAGGTTGC
 GGAAATAGTCAAGGACAAACAATAAATCAATACTAATACTCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCCCTCAAAATGTTAAT

SEQ ID NO. 8805

STRAIN COH1

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAGTT
 GTCTTAACCGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACATAATCGCA
 TTAGAACTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTTCC
 GTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCAAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAAAG
 GCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAACACAAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAATAAATCAATACTAATACTCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCCACCCCTCAAAATGTTAAT

SEQ ID NO. 8806

STRAIN M781

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAG
 TTGTCTTAACCGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACATAATCG
 CATTAGAAGTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTT
 CCGTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC
 ATATGCACATACAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAA
 AGGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATT
 CTAAAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACA
 AATTAAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAAAAATAAATCAACTGATAAAACACAACACAAAATGGTCAGGTTGC
 GGAAATAGTCAAGGACAAACAATAAATCAATACTAATACTCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCCCTCAAAATGTTAAT

SEQ ID NO. 8807

STRAIN CJB110

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAG
 TTGTCTTAACCGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACATAATCG
 CATTAGAAGTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTT
 CCGTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC

Table 88: Comparative Sequences relating to SAG0477

ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGAAACTGGAAAAA
 AGGCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCTGATTAAATAAGTGAGATTAGGTTAGCTGATT
 CTAACACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTACAAACA
 AATTAAAGAAAGCCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAATAATCAACTGATATAAACACAACACAATAATGGTCAGGTTGC
 GAAAAATAGTCAAGGACAAACAAATAACTCAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCCAACCTCAAAATGTTAAT

SEQ ID NO. 8808

STRAIN 1169NT

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAAGT
 TGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCA
 AAGAAGATGAAGAAGAACAACAAACGTATTACGAAAAATTACGCTTAGAT
 AAAAGAAGTAAATTAATATTTCTCTCTCTGAAGAACCTCAAAATACTAC
 TAAATTAAGAAGCTTCATTTTCCAAAGATTCAAAACCTAAGATTGAAA
 AGAAACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAACTAATCGC
 ATTAGAATCTGCACCTATATTATTAGTAGCATTCTAGTCATTTTAGTTTC
 CGTTTTCTACTAATCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTG
 GAAATCAGCATACACCTGATGATATTTTGATAGAGAAAAAGCAATATTCAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACA
 ACCTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATC
 AATTTCCCAACAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCA
 TATGCACATACAAAGCAAGGATATCAGCCTGTCTTGAAACTGGAAAAA
 GGCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTA
 ACCTTGATAAGGAAGATAGTATTAAAGCTATTAAATAAGATTAAAGGCT
 TTAGACCTGATTAAATAAGTGAGATTAGGTTGATAAGTTTAGCTGATT
 TAAAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTA
 TTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAA
 ATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGT
 TTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATA
 CAAAAATAAATCAACTGATATAAACACAACCCCAAAATGGTCAGGTTGCG
 GAAAAATAGTCAAGGACAAACAAATACTCAATACTAATCAACAAGGACA
 ACAACAGATAGCAACGAGCAGGCACCCCAACCTCAAAATGTTAAT

SEQ ID NO. 8809

STRAIN JM9130013

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAAGT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCA
 AGAAGATGAAGAAGAACAACAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTTCTCTCTCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAAAA
 GAAACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAACTAATCGCA
 TTAGAATCTGCACCTATATTTTAGTAGCATTCTAGTCATTTTAGTTTCC
 GTTTTCTACTAATCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTTGATAGAGAAAAAGCAATATTCAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGAAACTGGAAAAAAG
 CCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTA
 CCCTTGATAAGGAAGATAGTATTAAAGCTATTAAATAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTAGGTTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGT
 TACACAACAACAATAACCATTTGAATCAACCCCTGTTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATATAAACACAACACAATAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8810

STRAIN A909

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAAGTGTCT
 TTAACGGAATGGCAAAAGCGTAACCTTGAATTTTaaAAAAACGCAAGA
 AGATGAAGAAGAAaCAAAAAAGTATTAAAGCAAAAAATTACGCTTAGATAAAA
 GAAGTAATTAATATTTCTCTCTCTGAAGAACCTCAAAATACTACTAAA
 ATTAAGAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAAAAAGAA
 ACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAACTAATCGCATTA
 GAATGACACCTATATTGTTAGTAGCATTCTAGTCATTTTAGTTTCCGTT
 TTCTCTAATCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGGAAA
 TCAGCATACACCTGATGATATTTTGATAGAGAAAAAGCAATATTCAAAAA
 ACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAACGT
 TTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATT
 TCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCATATG
 CACATACAAAGCAAGGATATCAACCTGTCTTGAAACTGGAAAAAAGGCT
 GATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTAACCT
 TGATAAGGAAGATAGTATTAAAGCTATTAAATAAGATTAAAGGCTTTAG
 ACCCTGATTAAATAAGTGAGATTAGGTTGATAAGTTTAGCTGATTCTAAA
 ACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTATTAA

Table 88: Comparative Sequences relating to SAG0477

AATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAATTA
 AGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTAC
 ACAACAACAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATACAAA
 AAATAAATCAACTGATAAAACCAAAmCACAAAATGGTCAGGTTGCGGAAA
 ATAGTCAAGGACAAACAATAACTCAAATACTAATCAACAAGGACAACAG
 ATAGCAACAGAGCAGGCACCTAACCTCAAATGTTAAT

SEQ ID NO. 8811

STRAIN 090

TAAGAAGAAATCAGATACCCAGAAAAAGAAGTTGTCTTAACGGAAT
 GGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAAGAAGATGAAGAA
 GAACAAAACGTATTAAACGAAAAATTACGCTTAGATAAAAGAAGTaaATT
 AAATATTCTTCTCCTGAAGAACCTCAAATACTACTAAAATTAGAAGC
 TTCATTTTCCAAGATTTCAAAACCTAAGATTGAAAAGAAACAGAAAAAA
 GAAAAAATAGTCAACAGCTTAGCCAAAATTAATCGCATTAGAACTGCACC
 TATATTGTTAGTAGCATTCTTAGTCATTTTAGTTTCCGTTTTCCTACTAA
 CTCTTTTAGTAAGCAAAAACATAACAGTTAGTGGAAATCAGCATACA
 CCTGATGATATTTTGATAGAAAAACGAATATTCAAAAAACGATTATTT
 CTTTCTTTAATTTTAAACATAAAGCTATTGAACAACGTTTAGCTGCAG
 AAGATGTATGGGTA AAAACAGCTCAGATGACTTATCAATTTCCCAATAAG
 TTTCAATTTCAAGTTCAAGAAAAATAAGATTATTGCATATGCACATACAAA
 GCAAGGATATCAGCCTGTCTTGAAACTGGA AAAAGGCTGATCCTGTAA
 ATAGTTTCAGAGCTACCAAGCACTTCTTAACAATTAACCTTGATAAGGAA
 GATAGTATTAAGCTATTAATTAAGATTAAAGGCTTAGACCCGTGATTT
 AATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATTTAAAACGACACCTG
 ACCTCCTGCTGTTAGATATGATGATGGAATAGTATTAGAATACCATTA
 TCTAAATTTAAAGAAAGACTTCTCTTTTACAAACAAATTAAGAAGAACTT
 TAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAA
 GTACTATTGAATCAACCCCTGTGAAAGCGGAAGATACAAAAAATAAATCA
 ACTGATATAAAACAAACCAAAATGGTCAGGTTGCGGAAAATAGTCAAGG
 ACTAACAAATAACTCAAATACTAATCAACAAGGACAACAGATGCAACAG
 AGCAGGCACCAACCTCAAATGTTAAT

PRETTY of: /biotmp/msa24691.2{*} August 5, 2002 05:14 ..

	1	50
msa252409.2{85_090.con}	~~TAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_CJB110}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_COH1}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_M732}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_M781}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_18RS21}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_2603}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_A909}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_H36B}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_JM9130013}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_1169NT}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
Consensus	*****	*****
	51	100
msa252409.2{85_090.con}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_CJB110}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_COH1}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_M732}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_M781}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_18RS21}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_2603}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_A909}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_H36B}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_JM9130013}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_1169NT}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
Consensus	*****	*****
	101	150
msa252409.2{85_090.con}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_CJB110}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_COH1}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_M732}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_M781}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_18RS21}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_2603}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_A909}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_H36B}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_JM9130013}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_1169NT}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
Consensus	*****	*****
	151	200
msa252409.2{85_090.con}	TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	
msa252409.2{85_CJB110}	TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	
msa252409.2{85_COH1}	TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	
msa252409.2{85_M732}	TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_M781}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_18RS21}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_2603}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_A909}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_H36B}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_JM9130013}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_1169NT}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_CJB110}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_COH1}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_M732}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_M781}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_18RS21}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_2603}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_A909}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_H36B}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_JM9130013}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_1169NT}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
Consensus	*****	*****	***-*****	*****	*****
msa252409.2{85_090.con}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_CJB110}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_COH1}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_M732}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_M781}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_18RS21}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_2603}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_A909}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_H36B}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_JM9130013}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_1169NT}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_CJB110}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_COH1}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_M732}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_M781}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_18RS21}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_2603}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_A909}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_H36B}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_JM9130013}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_1169NT}	CCTATATTTa	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_CJB110}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_COH1}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_M732}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_M781}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_18RS21}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_2603}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_A909}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_H36B}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_JM9130013}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_1169NT}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_CJB110}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_COH1}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_M732}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_M781}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_18RS21}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_2603}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_A909}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_H36B}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_JM9130013}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_1169NT}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
Consensus	*****	*****	***-*****	*****	*****
msa252409.2{85_090.con}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_CJB110}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_COH1}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_M732}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_M781}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_18RS21}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_2603}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_A909}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_H36B}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_JM9130013}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_1169NT}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
Consensus	*****	*****	*****	*****	*****		
msa252409.2{85_090.con}	501	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	550
msa252409.2{85_CJB110}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_COH1}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_M732}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_M781}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_18RS21}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_2603}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_A909}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_H36B}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_JM9130013}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
msa252409.2{85_1169NT}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	TTTCCCAATa	
Consensus	*****	*****	*****	*****	*****	*****	
msa252409.2{85_090.con}	551	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	600
msa252409.2{85_CJB110}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_COH1}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_M732}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_M781}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_18RS21}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_2603}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_A909}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_H36B}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_JM9130013}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
msa252409.2{85_1169NT}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	TGCACATACA	
Consensus	*****	*****	*****	*****	*****	*****	
msa252409.2{85_090.con}	601	AAGCAAGGAT	ATCagCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	650
msa252409.2{85_CJB110}	AAGCAAGGAT	ATCagCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_COH1}	AAGCAAGGAT	ATCagCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_M732}	AAGCAAGGAT	ATCagCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_M781}	AAGCAAGGAT	ATCagCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_18RS21}	AAGCAAGGAT	ATCagCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_2603}	AAGCAAGGAT	ATCagCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_A909}	AAGCAAGGAT	ATCagCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_H36B}	AAGCAAGGAT	ATCagCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_JM9130013}	AAGCAAGGAT	ATCagCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
msa252409.2{85_1169NT}	AAGCAAGGAT	ATCagCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	CTGATCCTGT	
Consensus	*****	*****	*****	*****	*****	*****	
msa252409.2{85_090.con}	651	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	700
msa252409.2{85_CJB110}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_COH1}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_M732}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_M781}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_18RS21}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_2603}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_A909}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_H36B}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_JM9130013}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
msa252409.2{85_1169NT}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	CTTGATAAGG	
Consensus	*****	*****	*****	*****	*****	*****	
msa252409.2{85_090.con}	701	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	750
msa252409.2{85_CJB110}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	AGACCCCTGAT	
msa252409.2{85_COH1}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	AGACCCCTGAT	
msa252409.2{85_M732}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	AGACCCCTGAT	
msa252409.2{85_M781}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	AGACCCCTGAT	
msa252409.2{85_18RS21}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	AGACCCCTGAT	
msa252409.2{85_2603}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	AGACCCCTGAT	
msa252409.2{85_A909}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	AGACCCCTGAT	
msa252409.2{85_H36B}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	AGACCCCTGAT	
msa252409.2{85_JM9130013}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	AGACCCCTGAT	
msa252409.2{85_1169NT}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	AGACCCCTGAT	
Consensus	*****	*****	*****	*****	*****	*****	
msa252409.2{85_090.con}	751	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC	800
msa252409.2{85_CJB110}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC	AAACGACACC	

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_COH1}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_M732}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_M781}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_18RS21}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_2603}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_A909}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_H36B}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_JM9130013}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_1169NT}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_CJB110}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_COH1}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_M732}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_M781}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_18RS21}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_2603}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_A909}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_H36B}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_JM9130013}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_1169NT}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_CJB110}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_COH1}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_M732}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_M781}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_18RS21}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_2603}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_A909}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_H36B}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_JM9130013}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_1169NT}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_CJB110}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_COH1}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_M732}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_M781}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_18RS21}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_2603}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_A909}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_H36B}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_JM9130013}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_1169NT}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_CJB110}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_COH1}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_M732}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_M781}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_18RS21}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_2603}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_A909}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_H36B}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_JM9130013}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_1169NT}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
Consensus	**--***--***	*****	****-*****	-*****	*****
msa252409.2{85_090.con}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_CJB110}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_COH1}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_M732}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_M781}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_18RS21}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_2603}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_A909}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_H36B}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_JM9130013}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_1169NT}	CAACTGATAA	AACACAAaCc	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
Consensus	*****	*****-*	*****	*****	*****
msa252409.2{85_090.con}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_CJB110}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_COH1}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_M732}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_M781}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_18RS21}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_2603}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_A909}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_H36B}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_JM9130013}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_1169NT}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGGacaAC	AACAGATAGC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	1101				1134
msa252409.2{85_CJB110}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_COH1}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_M732}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_M781}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_18RS21}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_2603}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_A909}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_H36B}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_JM9130013}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_1169NT}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
Consensus	***-*****	*****-****	*****	****	

SEQ ID NO. 8812

STRAIN 2603 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEBPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPI FVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPPDILIEKTNI QKNDYFFSLI FKHKAI EQR LAEDVWVKTAQMTYQ
 FPNKFHI QVQENKI IAYAH TKQGYQPVLE TGKKADPVNSSEL PKHFLTINLDKEDSI KLL
 IKDLKALDPDLI SEIQV ISLADSKTTPDLLLLDMHDGNSIRI PLSKFKERLPFYKQIKKN
 LKEPSIVDMEVG VYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNNTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8813

STRAIN H36B frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEBPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPI FVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPPDILIEKTNI QKNDYFFSLI FKHKAI EQR LAEDVWVKTAQMTYQ
 FPNKFHI QVQENKI IAYAH TKQGYQPVLE TGKKADPVNSSEL PKHFLTINLDKEDSI KLL
 IKDLKALDPDLI SEIQV ISLADSKTTPDLLLLDMHDGNSIRI PLSKFKERLPFYKQIKKN
 LKEPSIVDMEVG VYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNNTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8814

STRAIN 18RS21 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEBPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPI FVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPPDILIEKTNI QKNDYFFSLI FKHKAI EQR LAEDVWVKTAQMTYQ
 FPNKFHI QVQENKI IAYAH TKQGYQPVLE TGKKADPVNSSEL PKHFLTINLDKEDSI KLL
 IKDLKALDPDLI SEIQV ISLADSKTTPDLLLLDMHDGNSIRI PLSKFKERLPFYKQIKKN
 LKEPSIVDMEVG VYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNNTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8815

STRAIN M732 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEBPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPI FVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPPDILIEKTNI QKNDYFFSLI FKHKAI EQR LAEDVWVKTAQMTYQ
 FPNKFHI QVQENKI IAYAH TKQGYQPVLE TGKKADPVNSSEL PKHFLTINLDKEDSI KLL
 IKDLKALDPDLI SEIQV ISLADSKTTPDLLLLDMHDGNSIRI PLSKFKERLPFYKQIKKN
 LKEPSIVDMEVG VYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNNTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8816

STRAIN COH1 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEBPQ
 NTTKI KKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPI FVVAFLVILVSVFLLTPF
 SKQKTI TVSGNQHTPPDILIEKTNI QKNDYFFSLI FKHKAI EQR LAEDVWVKTAQMTYQ
 FPNKFHI QVQENKI IAYAH TKQGYQPVLE TGKKADPVNSSEL PKHFLTINLDKEDSI KLL
 IKDLKALDPDLI SEIQV ISLADSKTTPDLLLLDMHDGNSIRI PLSKFKERLPFYKQIKKN
 LKEPSIVDMEVG VYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNNTNQ
 GQQQIATEQAPNPQNVN

SEQ ID NO. 8817

STRAIN M781 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEBPQ

Table 88: Comparative Sequences relating to SAG0477

NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8818

STRAIN CJB110 frame: 1

PKKKS DTPKEKEEVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEEQ
 NTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8819

STRAIN 1169NT frame: 1

PKKKS DTPKEKEEVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEEQ
 NTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8820

STRAIN JM9130013 frame: 1

PKKKS DTPKEKEEVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEEQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8821

STRAIN A909 frame: 1

PKKKS DTPKEKEEVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEEQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIXIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKS TDKTQXQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8822

STRAIN 090 frame: 2

KKKS DTPKEKEEVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEEQ
 TTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 KQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 PNKFHIQVQENKI IAYAHKQGYQPVLETGKKADPVNSSELPHFLTINLDKEDSIKLLI
 KDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKNL
 KEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKS TDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

PRETTY of: /biotmp/msa252337.2{*} January 31, 2003 03:32 ..

	1	50
msa252337.2{85_090}	-KKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_18RS21}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_2603}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_A909}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_CJB110}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_COH1}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_H36B}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_JM9130013}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_M732}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_M781}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_1169NT}	PKKKS DTPKEK	EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
Consensus	*****	*****
	51	100
msa252337.2{85_090}	LNISSEPEEQ	NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRIRTA
msa252337.2{85_18RS21}	LNISSEPEEQ	NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRIRTA
msa252337.2{85_2603}	LNISSEPEEQ	NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRIRTA
msa252337.2{85_A909}	LNISSEPEEQ	NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRIRTA
msa252337.2{85_CJB110}	LNISSEPEEQ	NTTKIKKLHF PKISrPKIEK QKQKEKIVNS LAKTNRIRTA

Table 88: Comparative Sequences relating to SAG0477

msa252337.2{85_COH1}	LNISSPPEEPQ	NTTKIKKLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_H36B}	LNISSPPEEPQ	NTTKIKKLHF	PKISrPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_JM9130013}	LNISSPPEEPQ	NTTKIKKLHF	PKISrPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_M732}	LNISSPPEEPQ	NTTKIKKLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_M781}	LNISSPPEEPQ	NTTKIKKLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_1169NT}	LNISSPPEEPQ	NTTKIKKLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
Consensus	*****	*****	****_*****	*****	*****
msa252337.2{85_090}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_18RS21}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_2603}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_A909}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_CJB110}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_COH1}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_H36B}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_JM9130013}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_M732}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_M781}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_1169NT}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
Consensus	***_*****	*****	*****	*****	*****
msa252337.2{85_090}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_18RS21}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_2603}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_A909}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_CJB110}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_COH1}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_H36B}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_JM9130013}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_M732}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_M781}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_1169NT}	FFSLIFKHKA	IEORLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
Consensus	*****	*****	*****	*****	*****
msa252337.2{85_090}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_18RS21}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_2603}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_A909}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_CJB110}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_COH1}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_H36B}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_JM9130013}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_M732}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_M781}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_1169NT}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
Consensus	*****	*****	*****	*****	*****
msa252337.2{85_090}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_18RS21}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_2603}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_A909}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	xIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_CJB110}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_COH1}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_H36B}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_JM9130013}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_M732}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_M781}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
msa252337.2{85_1169NT}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFFYKQIKKN
Consensus	*****	*****	*****	-*****	*****
msa252337.2{85_090}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_18RS21}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_2603}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_A909}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQx	QNGQVAENSQ
msa252337.2{85_CJB110}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_COH1}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_H36B}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_JM9130013}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_M732}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_M781}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_1169NT}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
Consensus	*****	*****_**	*****	*****_	*****
msa252337.2{85_090}	GQTNNNSNTNQ	QGQQiatega	pnpqnv-		
msa252337.2{85_18RS21}	GQTNNNSNTNQ	QGQQiatega	pnpqnv-		
msa252337.2{85_2603}	GQTNNNSNTNQ	QGQQiatega	pnpqnv-		
msa252337.2{85_A909}	GQTNNNSNTNQ	QGQQiatega	pnpqnv-		

Table 88: Comparative Sequences relating to SAG0477

msa252337.2{85_CJB110}	GQTNNSENTNQ	QGQQiateqa	pnpgnvn~
msa252337.2{85_COH1}	GQTNNSENTNQ	QGQQiateqa	pnpgnvn~
msa252337.2{85_H36B}	GQTNNSENTNQ	QGQQiateqa	pnpgnvn~
msa252337.2{85_JM9130013}	GQTNNSENTNQ	QGQQiateqa	pnpgnvn~
msa252337.2{85_M732}	GQTNNSENTNQ	QGQQiateqa	pnpgnvn~
msa252337.2{85_M781}	GQTNNSENTNQ	QGQQiateqa	pnpgnvn~
msa252337.2{85_1169NT}	GQTNNSENTNQ	QGQQiateq	apnpgnvn
Consensus	*****	****~-----	-----*

Table 89: Comparative Sequences relating to SAG1350

SEQ ID NO. 8901

STRAIN 2603

ATGAAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTCTACGTAAA
 TATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTACATAATGGTCACAAGTCCTGTT
 TTTGCGGATCAAACACATCGGTTCAAGTTAATAATCAGACAGGCACCTAGTGTGGATGCT
 AATAATTCCTCCAATGAGACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGT
 CAAGCGTCTGATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
 TTAGTAGAGACAAAGCCAAATGGTGGAAAAACATTACCTGAACAAGGGAATTTATGTTTAT
 AGCAAGAAACCGAGGTGAAAAATACACCTTCAAATCAGCCCCAGTAGCTTTCTATGCA
 AAGAAAGGTGATAAAGTTTCTATGACCAAGTATTTAATAAAGATAATGTGAAATGGATT
 TCATATAAGTCTTTTGTGGCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCA
 GGAGGTTTCAGAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTTATACATTTTCACATAAAGTAGAAGTAAAAAATGAAGCT
 AAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGACAGAATTTTTTACGACCAA
 ATACTAACTATTGAAGGAAATCAGTGGTTATCTTATAAATCAITCAATGGTGTCTCGTCT
 TTTGTTTGTCTAGGTAAAGCATCTTCAGTAGAAAAAATGAAGATAAAGAAAAAGTGTCT
 CCTCAACCACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACT
 ACAGGTTTTGATATTTTAAATACGAATATTAAAGATGATAACGGTATCGTGTCTGTTAAG
 GTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATTAAATGGTATACAGCTGTAAC
 ACTGGGGATGGCAACTACAAAGTAGCTGTATCATTTGCTGACCATAAGAATGAGAAGGGT
 CTTTATAATATTCTTTTACTACCAAGAGCTAGTGGGACACTTGTAGGTGTAAACAGGA
 ACTAAAGTGACAGTAGCTGGAACTAATTTCTCTCAAGAACCTATTGAAAAAGGTTTAGCA
 AAGACTGGTGTTTTAAATATTATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAAATATCA
 AGTCAGACCCAAATTTACTTTAGAAAAAGGTGACAAAAATAAATATGATCAAGTATTGACA
 GCAGATGGTTTACCAGTGGATTCTTACAAATCTTATAGTGGTGTTCGTGCTATATTCCT
 GTGAAAAAGCTAACTACAGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGT
 TATCCCACTTACCTTAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAAATACATTAT
 GATCAAGTGTTAGTAGTAGATGGTTCATCAGTGGATTTTCATACAAGAGTTATTCGGTATT
 CGTCGCTATATTGAAAT

SEQ ID NO. 8902

STRAIN 090

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
 CTCTACGTAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
 ATAATGGTCACAAGTCTCTGTTTGTGCGGATCAAACACATCGGTTCAAGT
 TAATAATCAGACAGGCACCTAGTGTGGATGCTAATAATCTTCCAATGAGA
 CAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 GATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
 TTTAGTAGAGACAAAGCCAAATGGTGGAAAAACATTACCTGAACAAGGGA
 ATTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAATCA
 GCCCCAGTAGCTTTCTATGCAAAAGAAAGGTGATAAAGTTTCTATGACCA
 AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTG
 GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
 GAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGA
 GAAAAATAGCAACGCAAGGAAATATACATTTTCACATAAAGTAGAAGTAA
 ABAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGA
 ACAGAAATTTTACGACCAAAATACTAACTATTGAAGGAAATCAGTGGTT
 ATCTTATAAATCAITCAATGGTGTTCGTGTTTGTCTAGGTAAAG
 CATCTTCAGTAGAAAAAATGAAGATAAAGAAAAAGTGTCTCCTCAACCA
 CAAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAACT
 TACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCG
 CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATT
 AAATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGT
 ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCAITTTAT
 ACTACAGAAGCTAGTGGGACACTTGTAGGTGTAAACAGGAACATAAGTG
 ACAGTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAATGGTTTAGC
 AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAATGAAG
 CTAAAAATATCAAGTCAAGTCAAGCCCAATTTACTTTAGAAAAAGGTGACAAAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTCTTACAA
 ATCTTATAGTGGTGTTCGTGCTATATTCCTGTGAAAAAGCTAACTACAA
 GTAGTAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
 TTACCTAAAAAGGTACCTATACATTTACTAAAACTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTCAAAGGGTGAAA
 AAATACATTATGATCAAGTGTAGTAGTAGATGGTTCATCAGTGGATTTCA
 TACAAGAGTTATTCGGTATTCGTGCTATATTGAAAT

SEQ ID NO. 8903

STRAIN A909

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTAC
 TCCTACGTAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
 CATATAATGGTCACAAGTCTCTGTTTGTGCGGATCAAACACATCGGTTCAAG
 TTAATAATCAGACAGGCACCTAGTGTGGATGCTAATAATCTTCCAATGAG
 ACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 TGATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTC
 CTTTAGTAGAGACAAAGCCAAATGGTGGAAAAACATTACCTGAACAAGGG
 AATTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAATC
 AGCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACC
 AAGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGT
 GCGGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTT
 AGAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAG
 AGAAAAATAGCAACGCAAGGAAATTTATACATTTTCACATAAAGTAGAAGTA
 AAAAAAGGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGG

Table 89: Comparative Sequences relating to SAG1350

AGACAGAATTTTTTACGACCAAATACTAATCTATTGAAGGAAATCAGTGGT
TATCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAA
GCATCTTCAGTAGAAAAAAGCTGAAGATAAAGAAAAAGTGTCTCCTCAACC
ACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAA
CTACAGGTTTTGATATTTAATTACGAATATTAAGATGATAACGGTATC
GCTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATAT
TAAATGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTG
TATCATTTGCTGACCATAAGAAATGAGAAGGGTCTTTATAATATTCAATTA
TACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGT
GACAGTAGCTGGAATAATCTTCTCAAGAACCCTATTGAAATGGTTTAG
CAAAGACTGGTGTATTATAATATTATCGAAGTACTGAAGTAAAAAATGAA
GCTAAAATATCAAGTCAGACCCCAATTTACTTTAGAAAAAGGTGACAAAAT
AAATTTATGATCAAGTATTGACAGCAGATGGTTACAGTGGATTCTTACA
AATCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACA
AGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAA
CTTACCTAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGA
GTCACCTAAAAGTATCAAGTCCAGTGGAAATTAATTTTCAAAGGGTGAA
AAAAATACATTATGATCAAGTGTAGTAGATGGTCATCAGTGGATTTC
ATACAAGAGTTATTCCGGTATTCTGTCGTATATTGAAATT

SEQ ID NO. 8904

STRAIN H36B

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
CTCTACGTAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTTC
ATAATGGTCAACAAGTCTGTGTTTTGCGGATCAAACTACATCGGTTCAAGT
TAATAATCAGACAGGCACTAGTGTGGATGATAAATTTCTTCCAATGAGA
CAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCT
GATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
TTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAGGGA
ATTATGTTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCA
GCCCCAGTAGCTTTCTATGCAAGAAGGATGATAAAGTTTTCTATGACCA
AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTG
GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
GAGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGA
GAAAAATAGCAACGCAAGGAAATATACATTTTACATAAAGTAGAAGTAA
AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGA
GACAGAATTTTTTACGACCAAAATACTAATTTGAAGGAAATCAGTGGTT
ATCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAAG
CATCTTCAGTAGAAAAAAGCTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
CAAGCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAAAC
TACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCG
CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
AAATGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTGT
ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCAATTAT
ACTACCAAGAAAGCTAGTGGGACACTTGTAGGTGTAACAGCACTAAAGTG
ACAGTAGCTGGAACCAATCTTCTCAAGAACCCTATTGAAAATGGTTTTAGC
AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
CTAAAATATCAAGTCAGACCCCAATTTACTTTAGAAAAAGGTGACAAAATA
AATTATGATCAAGTATTGACAGCAGATGGTTACAGTGGATTCTTACAA
ATCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAA
GTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
TTACCTAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGAG
TCAACCTAAAAGTATCAAGTCCAGTGGAAATTAATTTTCAAAGGGTGAAA
AAATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTC
TACAAGAGTTATTCCGGTATTCTGTCGTATATTGAAATT

SEQ ID NO. 8905

STRAIN 18RS21

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTC
TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCA
TAATGGTCAACAAGTCTGTGTTTTGCGGATCAAACTACATCGGTTCAAGTT
AATAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGAC
AAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTG
ATAAAGTTGTAATAAGTCAAAATACGGCAACAAAGGACATTACTACTCT
TTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAGGGAA
TTATGTTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAG
CCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCAA
GTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTGG
CGTAGCTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTGAG
AGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
AAAATAGCAACGCAAGGAAATATACATTTTACATAAAGTAGAAGTAAA
AAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGCAAAAGGAG
ACAGAATTTTTTACGACCAAAATACTAATTTGAAGGAAATCAGTGGTTA
TCATTATAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAAGC
ATCTTCAGTAGAAAAAAGCTGAAGATAAAGAAAAAGTGTCTCTCAACCAC
AAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACT
ACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCGC
TGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTA
AATGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTGTA
TCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCAATTTATA
CTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTGA
CAGTAGCTGGAACCAATCTTCTCAAGAACCTATTGAAAAAGGTTTAGCA
AAGACTGGTGTATTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGC

Table 89: Comparative Sequences relating to SAG1350

TAAAAATCAAGTCAGACCCCAATTTACTTTAGAAAAAGGTGACAAAATAA
 ATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAAA
 TCTTATAGTGGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAAG
 TAGTGA AAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACT
 TACCTAAAACAGGTACCTATACATTTACTAAAACGTAGATGTGAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAAAGGTGAAAA
 AATACHTTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTTCAT
 ACAAGAGTTATTCCGGTATTTCGTGCTATATTGAAATT

SEQ ID NO. 8906

STRAIN M732

CAAGTAAATGATaCTAAGCAATCTTACTCTCTACGTAAATATAAATTGCG
 TTTAGCATCAGTAATTTTAGGGTCATTCTATAATGGTCACAAGTCCGTGTT
 TTGCGGATCAAACTACATCGGTTCAAGTTAATAATCAGACAGGCACTAGT
 GTGGATGCTAATAATTCTTCCAATGAGACAAGTCCGTCAAGTGTGATTAC
 TTCCAATATGATAGTGTCAAGCGTCTGATAAAGTTGTAAATAGTCAAA
 ATACGGCAACAAAGGACATTACTACTCCTTTAGTAGAGACAAAGCCAATG
 GTGGA AAAACATTTACCTGAACAAGGGAATTTATGTTTATAGCAAGA AAC
 CGAGGTGAAAAATACACCTTCAAAATCAGCCCCAGTAGCTTTCTATGCAA
 AGAAAGGTGATAAAGTTTCTATGACCAAGTATTTAATAAAGATAATGTG
 AAATGGATTTATATAAGTCTTTTGGTGGCGTACGTGATACGCAGCTAT
 TGAGTCACTAGATCCATCAGGAGGTTTCAAGAGCTAAAGCACCTACTCCTG
 TAACAAATTCAGGAAGCAATAATCAAGAGAAAATAGCAACGCAAGGAAAT
 TATACATTTTACATAAAGTAGAAGTAAAAATGAAGCTAAGGTAGCGAG
 TCCAATCAATTTTACATTTGGACAAAGGAGACAGAATTTTACGACCAAA
 TACTAATCTatTGAAGGAAATCAGTGGTTATCTTATAAATCATTCATGGT
 GTTCGTGCTTTTGTtTtGcTAGGTAAGCATCTTCAGTAGAAAAAACTGA
 AGATAAAGAAAAAGTGTCTCTCAACCAAGCCGTATTACTAAAACCTG
 GTAGACTGACTATTTCTAACGAAACAACTACAGGTTTGTATATTTAATT
 ACGAATATTAAGATGATAACGGTATCGCTGCTGTTAAGGTACCGGTTTG
 GACTGAACAGGAGGCGCAAGATGATTAATAGTATACAGCTGTAACATA
 CTGGGGATGGCAACTACAAAGTAGCTGTATCATTTGCTGACCATAGAAT
 GAGAAGGGTCTTTATAAATTTCAATTTATACTACCAAGAAGCTAGTGGGAC
 ACTTGTAGGTGTAAACAGGAACATAAGTGACAGTAGCTGGAACATAATCTT
 CTCAAGAACCTATTGAAAATGGTTTACCAAGACTGGTGTTTATAATATT
 ATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAAATATCAAGTCAGACCCA
 ATTTACTTTAGAAAAAGGTGACAAAATAAATTATGATCAAGTATTGACAG
 CAGATGGTTTACCAGTGGATTCTTACAAATCTTATAGTGGTGTTCGTGCG
 TATATTTCTGTGAAAAAGCTAACTACAAGTAGTGA AAAAGCGAAAGATGA
 GGCGACTAAACCGACTAGTTATCCCAACTTACCTAAACAGGTACCTATA
 CATTTACTAAAACGTAGATGTGAAAAGTCAACCTAAAGTATCAAGTCCA
 GTGGAATTTAATTTTCAAAAAGGTGAAAAATACATTATGATCAAGTGT
 AGTAGTAGATGGTCATCAGTGGATTTCATACAAAGATTATTCCGGTATTC
 GTCGCTATATTGAAATT

SEQ ID NO. 8907

STRAIN COH1

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTCT
 ACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCTATAA
 TGGTCACAAGTCCGTGTTTTCGCGATCAAACTACATCGGTTCAAGTTAAT
 AATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGACAAG
 TGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTGATA
 AAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCTTTA
 GTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGGAATTA
 TGTTTATAGCAAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAGCCC
 CAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGACCAAGTA
 TTTAATAAAGATAATGTTAAATGGATTTCATATAAGTCTTTGGTGGCGT
 ACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAGAGA
 CTAAGACACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGAGAAA
 ATAGCAACGCAAGGAAATTTATACATTTTACATAAAGTAGAAGTAaAAAA
 TGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGACA
 GAATTTTTTACGACCAATACTAATCTATTGAAGGAAATCAGTGGTTATCT
 TATAAATCATTTCAATGGTGTTCGTGCTTTTGTtTGCTAGGTAAAGCATC
 TTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCTCAACCAAG
 CCCGTTTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACTACA
 GGTTTTGTATTTTAAATTCGAATATTAAAGATGATAACGGTATCGCTGC
 TGTTAAGGTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATTAAAT
 GGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGTATCA
 TTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCAATTTATACTA
 CCAAGAAGCTAGTGGGACACTTGTAGGTGAACAGGAACATAAGTGACAG
 TAGCTGGAACATAATCTTCTCAAGAACCTATTGAAAAATGGTTTACCAAG
 ACTGGTGTTTATAATATATCGGAAGTACTGAAGTAAAAAATGAAGCTAA
 AATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATAAAT
 ATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTCTTACAAATCT
 TATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAAGTAG
 TGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTAC
 CTAAAACAGGTACCTATACATTTACTAAAACGTAGATGTGAAAAGTCAA
 CCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAAAGGTGAAAAAT
 ACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTCATACA
 AGAGTTATTCCGGTATTTCGTGCTATATTGAAATT

SEQ ID NO. 8908

STRAIN M781

Table 89: Comparative Sequences relating to SAG1350

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTT
 ACTCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCA
 TTCATAATGGTCAACAAGTCTGTCTTTTGGGATCAAACCTACATCGGTTCA
 AGTTAATAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATG
 AGACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCG
 TCTGATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTAC
 TCCTTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAG
 GGAATTATGTTTATAGCAAAAGAAACCGAGGTGAAAAATACACCTTCAAAA
 TCAGCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGA
 CCAAGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTG
 GTGGCGTACGTGATACGACGCTATTGAGTCACTAGATCCATCAGGAGGT
 TCAGAGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCA
 AGAGAAAATAGCAACGCAAGGAAATATACATTTTCACTATAAGTAGAAG
 TAAAAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAA
 GGAGACAGAAATTTTACGACCAAACTACTAATTTGAAGGAAATCAGTG
 GTTATCTTATAAATCATTTCAATGGTGTTCGTCGTTTGTGTTTGTAGGTA
 AAGCATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAA
 CCACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAAC
 AACTACAGGTTTGTATATTTAATTACGAATATTAAAGATGATAACGGTA
 TCGCTGCTGTTAAGGTACCGGTTTGGACTGAACAGGAGGGCAAGATGAT
 ATTAATGGTATACAGCTGTAACTACTGGGGATGGCACTACAAAGTAGC
 TGTATCATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCTATT
 TATACACCAAGAAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAA
 GTGACAGTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAATGGTTT
 ACCAAAGACTGGTGTATATAATATTATCGGAAGTACTGAAGTAAAAATG
 AAGCTAAAATATCAAGTCAGACCAATTTACTTTAGAAAAAGGTGACAAA
 ATAAATTTAGTATCAAGTATTTGACAGCAGATGGTTACCAAGTGGATTTCTTA
 CAAATCTTATAGTGGTGTTCGTCGCTATATCTCTGTGAAAAAGCTAACTA
 CAGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCC
 AACTTACCTAAAACAGGTACCTATACATTTTACTAAAACGTAGATGTGAA
 AAGTCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTG
 AAAAAATACATTATGATCAAGTGTAGTAGTAGATGGTCACTAGTGGATT
 TCATACAAGAGTTATTCGGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8909

STRAIN CJB110

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTCTC
 TACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTATA
 ATGGTCAACAAGTCTGTCTTTTGGGATCAAACCTACATCGGTTCAAGTTAA
 TAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGACAA
 GTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCTGAT
 AAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCTTT
 AGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAAGGGAAT
 ATGTTTATAGCAAAAGAACCGAGGTGAAAAATACACCTTCAAAATCAGCC
 CCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGACCAAGT
 ATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGTGGCG
 TACGTCGATACGACGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAGAG
 ACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAGAA
 AATAGCAACGCAAGGAAATATACATTTTCACTAAAGTAGAAGTAAAAA
 ATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGAC
 AGAATTTTTCAGACCAAAATATACTAATTTGAAGGAAATCAGTGGTTATC
 TTATAAATCATTTCAATGGTGTTCGTCGTTTGTGTTTGTAGGTAAAGCAT
 CTTCAAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCTCAACCCACAA
 GCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACTAC
 AGGTTTGTATATTTAATTACGAATATTAAAGATGATAACGGTATCGCTG
 CTGTTAAGGTACCGGTTTGGACTGAACAGGAGGGCAAGATGATATTA
 TGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTGTATC
 ATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCAATTTACT
 ACCAAGAAGCTAGTGGGACACTTGTAGGTGTACAGGAACCTAAAGTGACA
 GTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAATGGTTTAGCAAA
 GACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGCTA
 AAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATAAAT
 TATGATCAAGTATTGACAGCAGATGGTTACCAAGTGGATTCTTACAAATC
 TTATAGTGGTGTTCGTCGCTATATTCTGTGAAAAAGCTAACTACAAAGTA
 GTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTA
 CCTAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGAGTCA
 ACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAAAA
 TACATTATGATCAAGTGTAGTAGTAGATGGTCACTAGTGGATTTCATAC
 AAGAGTTATTCGGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8910

STRAIN 1169NT

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTC
 TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCA
 TAATGGTCAACAAGTCTGTCTTTTGGGATCAAACCTACATCGGTTCAAGTT
 AATAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGAC
 AAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCTG
 ATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
 TTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAAGGAA
 TTATGTTTATAGCAAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAG
 CCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGACCAA
 GTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGGTGG
 CGTACGTCGATACGACGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAG

Table 89: Comparative Sequences relating to SAG1350

AGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTTATACATTTTCACATAAAGTAGAAGTAAA
 AAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAG
 ACAGAATTTTACGACCAATATACTAATTTGAAGGAAATCAGTGGTTA
 TCTTATAAATCAATCAATGGTGTTCGTGTTTTGTTTTGCTAGGTAAAGC
 ATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCTCAACCAC
 AAGCCCGTATTACTAAACTGGTAGACTGACTATTTCTAACGAAACCACT
 ACAGGTTTTGATATTTAATTAACGAATATTAAGATGATAACGGTATCGC
 TGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATTA
 AATGGTATACAGCTGTAACACTGGGGATGGCAACTACAAAGTAGCTGTA
 TCATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCATTTATA
 CTACCAAGAGCTAGTGGGACACTTGTAGGTGTAACAGGAATAAAGTGA
 CAGTAGCTGGAaCTAATTCCTCTCAAGAACCTATTGAAAAAGGTTAGCA
 AAGACTGGTGTATTATAATATTCGGAAGTACTGAAGTAAAAATGAAGC
 TAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATAA
 ATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTCTTACAAA
 TCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAAG
 TAGTGA AAAAGCGAAGATGAGGCGACTAAACCGACTAGTTATCCCACT
 TACCTAAAACAGGTACCTATACATTTACTAAAAGTGTAGATGTGAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAA
 AATACATTATGATCAAGTGTAGTAGTAGTGGTCATCAGTGGATTTCAT
 ACAAGAGTTATTCGGTATTTCGTGCTATATTGAAATT

SEQ ID NO. 8911

STRAIN JM9130013

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
 CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTC
 ATAATGGTCACAAGTCTCTGTTTTGCGGATCAAACATACGCGTTCAAGT
 TAATAATCAGACAGGCACCTAGTGTGGATGCTAATAATTTCTTCAATGAGA
 CAAGTGCCTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 GATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
 TTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTTACCTGAACAAGGGA
 ATTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAATCA
 GCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCA
 AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGTG
 GCGTACGTCGATACGAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
 GAGACTAAAGCACCTACTCTCTGTAACAAATTCAGGAAGCAATAATCAAGA
 GAAATAGCAACGCAAGGAAATTTATACATTTTTCACATAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCCAACTCAATTTACATTGGACAAAGGA
 GACAGAATTTTTCAGCAACAAATACTAATTTGAAGGAATCAGTGGTT
 ATCTTATAAATCATTCATGGTGTTCGTGTTTTGTTTTGCTAGGTAAAG
 CATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
 CAAGCCCGTATTACTAAAAGTGGTAGACTGACTATTTATAACGAAACCAAC
 TACAGGTTTTGATATTTAATTACGAATATAAAGATGATAACGGTATCG
 TCGCTTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
 AAATGGTATACAGCTGTAACCTACTGGGGATGGCAACTACAAAGTAGCTGT
 ATCATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCATTTAT
 ACTACCAAGAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTG
 ACAGTAGCTGGAACTAATTTCTCTCAAGAACCTATTGAAAAAGGTTTAGC
 AAAGACTGGTGTATTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
 CTAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTCTTTACAA
 ATCTTATAGTGGTGTTCGTGCTATATTCTCTGAAAAAGCTAACTACAA
 GTAGTGAAAAAGCGAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
 TTACCTAAAACAGGTACCTATACATTTACTAAAAGTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAA
 AAATACATTATGATCAAGTGTAGTAGTAGTGGTCATCAGTGGATTTCAT
 TACAAGAGTTATTCGGTATTTCGTGCTATATTGAAATT

PRETTY of: /biotmp/msa255059.2{*} February 11, 2003 08:41 ..

	1		50
msa255059.2{91_M732}	----- --CAAGTAAA	TGATACTAAG	CAATCTTACT CTCTACGTAA
msa255059.2{91_M781}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_COH1}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_18RS21}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_2603}	atgAAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_1169NT}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_090}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_A909}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_CJB110}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_H36B}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_JM9130013}	---AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
Consensus	*****	*****	*****

	51		100
msa255059.2{91_M732}	ATATAAATTT	GGTTAGCAT	CAGTAATTTT AGGGTCATTC ATAATGGTCA
msa255059.2{91_M781}	ATATAAATTT	GGTTAGCAT	CAGTAATTTT AGGGTCATTC ATAATGGTCA
msa255059.2{91_COH1}	ATATAAATTT	GGTTAGCAT	CAGTAATTTT AGGGTCATTC ATAATGGTCA
msa255059.2{91_18RS21}	ATATAAATTT	GGTTAGCAT	CAGTAATTTT AGGGTCATTC ATAATGGTCA
msa255059.2{91_2603}	ATATAAATTT	GGTTAGCAT	CAGTAATTTT AGGGTCATTC ATAATGGTCA
msa255059.2{91_1169NT}	ATATAAATTT	GGTTAGCAT	CAGTAATTTT AGGGTCATTC ATAATGGTCA

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_090}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_A909}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_CJB110}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_H36B}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_JM9130013}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_M781}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_COH1}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_18RS21}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_2603}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_1169NT}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_090}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_A909}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_CJB110}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_H36B}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_JM9130013}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_M781}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_COH1}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_18RS21}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_2603}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_1169NT}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_090}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_A909}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_CJB110}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_H36B}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_JM9130013}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_M781}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_COH1}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_18RS21}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_2603}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_1169NT}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_090}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_A909}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_CJB110}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_H36B}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_JM9130013}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_M781}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_COH1}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_18RS21}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_2603}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_1169NT}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_090}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_A909}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_CJB110}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_H36B}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_JM9130013}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_M781}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_COH1}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_18RS21}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_2603}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_1169NT}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_090}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_A909}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_CJB110}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_H36B}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_JM9130013}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_M781}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_COH1}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_18RS21}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_2603}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_1169NT}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_090}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_A909}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_CJB110}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_H36B}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_JM9130013}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
Consensus	*****	*****	*****	*****	*****
	401				450
msa255059.2{91_M732}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_M781}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_COH1}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_18RS21}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_2603}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_1169NT}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_090}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_A909}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_CJB110}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_H36B}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_JM9130013}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
Consensus	*****	*****	*****	*****	*****
	451				500
msa255059.2{91_M732}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCITTTtGTG	GCGTACGTCG
msa255059.2{91_M781}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCITTTtGTG	GCGTACGTCG
msa255059.2{91_COH1}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCITTTtGTG	GCGTACGTCG
msa255059.2{91_18RS21}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCITTTtGTG	GCGTACGTCG
msa255059.2{91_2603}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCITTTtGTG	GCGTACGTCG
msa255059.2{91_1169NT}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCITTTtGTG	GCGTACGTCG
msa255059.2{91_090}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCITTTtGTG	GCGTACGTCG
msa255059.2{91_A909}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCITTTtGTG	GCGTACGTCG
msa255059.2{91_CJB110}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCITTTtGTG	GCGTACGTCG
msa255059.2{91_H36B}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCITTTtGTG	GCGTACGTCG
msa255059.2{91_JM9130013}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCITTTtGTG	GCGTACGTCG
Consensus	*****	*..*****	*****	*****_***	*****
	501				550
msa255059.2{91_M732}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_M781}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_COH1}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_18RS21}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_2603}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_1169NT}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_090}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_A909}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_CJB110}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_H36B}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_JM9130013}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
Consensus	*****	*****	*****	*****	*****
	551				600
msa255059.2{91_M732}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_M781}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_COH1}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_18RS21}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_2603}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_1169NT}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_090}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_A909}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_CJB110}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_H36B}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_JM9130013}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
Consensus	*****	*****	*****	*****	*****
	601				650
msa255059.2{91_M732}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_M781}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_COH1}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_18RS21}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_2603}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_1169NT}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_090}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_A909}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_CJB110}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_H36B}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_JM9130013}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
Consensus	*****	*****	*****	*****	*****
	651				700
msa255059.2{91_M732}	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_M781}	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_COH1}	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_18RS21}	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_2603}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_1169NT}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_090}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_A909}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_CJB110}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_H36B}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_JM9130013}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_M781}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_COH1}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_18RS21}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_2603}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_1169NT}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_090}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_A909}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_CJB110}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_H36B}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_JM9130013}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_M781}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_COH1}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_18RS21}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_2603}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_1169NT}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_090}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_A909}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_CJB110}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_H36B}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_JM9130013}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_M781}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_COH1}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_18RS21}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_2603}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_1169NT}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_090}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_A909}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_CJB110}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_H36B}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_JM9130013}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_M781}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_COH1}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_18RS21}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_2603}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_1169NT}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_090}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_A909}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_CJB110}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_H36B}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_JM9130013}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_M781}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_COH1}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_18RS21}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_2603}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_1169NT}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_090}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_A909}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_CJB110}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_H36B}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_JM9130013}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_M781}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_COH1}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_18RS21}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_2603}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_1169NT}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_090}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_A909}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_CJB110}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_H36B}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_JM9130013}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_M781}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_COH1}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_18RS21}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_2603}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_1169NT}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_090}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_A909}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_CJB110}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_H36B}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_JM9130013}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_M781}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_COH1}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_18RS21}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_2603}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_1169NT}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_090}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_A909}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_CJB110}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_H36B}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_JM9130013}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_M781}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_COH1}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_18RS21}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_2603}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_1169NT}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_090}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_A909}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_CJB110}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_H36B}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_JM9130013}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GAACCTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_M781}	GAACCTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_COH1}	GAACCTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_18RS21}	GAACCTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_2603}	GAACCTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_1169NT}	GAACCTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_090}	GAACCTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_A909}	GAACCTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_CJB110}	GAACCTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_H36B}	GAACCTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_JM9130013}	GAACCTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_M781}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_COH1}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_18RS21}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_2603}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_1169NT}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_090}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_A909}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_CJB110}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_H36B}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_JM9130013}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_M781}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC

msa255059.2{91_COH1}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_18RS21}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_2603}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_1169NT}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_A909}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_CJB110}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_H36B}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_JM9130013}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1301	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_M781}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_COH1}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_18RS21}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_2603}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_1169NT}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_A909}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_CJB110}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_H36B}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_JM9130013}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1351	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_M781}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_COH1}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_18RS21}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_2603}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_1169NT}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_A909}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_CJB110}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_H36B}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_JM9130013}	GGTGTTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1401	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_M781}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_COH1}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_18RS21}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_2603}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_1169NT}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_A909}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_CJB110}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_H36B}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_JM9130013}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1451	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_M781}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_COH1}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_18RS21}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_2603}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_1169NT}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_A909}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_CJB110}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_H36B}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_JM9130013}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1501	CAGTGAaATT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
msa255059.2{91_M781}	GTATCAAGTC	CAGTGAaATT	TAATTTTCAA		

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_M781}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_COH1}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_18RS21}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_2603}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_1169NT}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_090}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_A909}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_CJB110}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_H36B}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_JM9130013}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
Consensus	*****	*****	*****	*****	*****

msa255059.2{91_M732}	1601	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT	1629
msa255059.2{91_M781}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_COH1}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_18RS21}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_2603}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_1169NT}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_090}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_A909}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_CJB110}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_H36B}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_JM9130013}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
Consensus	*****	*****	*****		

SEQ ID NO. 8912

STRAIN 2603 frame: 1

MKKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQTGTSVDANNSS
 SNETSASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYYSKE
 TEVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVQWISYKSFQGVRRYAAIESLDPGGSS
 ETKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 DILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
 IHLYYQASGTLVGVTGKVTVAGTNSSQEPFENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLADGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8913

STRAIN 090 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYYSKET
 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVQWISYKSFQGVRRYAAIESLDPGGSE
 TKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
 HLYYQASGTLVGVTGKVTVAGTNSSQEPFENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLADGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8914

STRAIN A909 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYYSKET
 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVQWISYKSFQGVRRYAAIESLDPGGSE
 TKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
 HLYYQASGTLVGVTGKVTVAGTNSSQEPFENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLADGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8915

STRAIN H36B frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYYSKET
 EVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVQWISYKSFQGVRRYAAIESLDPGGSE
 TKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
 HLYYQASGTLVGVTGKVTVAGTNSSQEPFENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLADGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8916

STRAIN 18RS21 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYYSKET

Table 89: Comparative Sequences relating to SAG1350

EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAIVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8917

STRAIN M732 frame: 1

QVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSSNET
SASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKETEVK
NTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAIVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHNEKGLYNIHLY
YQEASGTLVGVTGKVTVAGTNSSQEPINENGLPKTGNYNIIGSTEVKNEAKISSQTQFTL
EKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
GTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYIEI

SEQ ID NO. 8918

STRAIN COH1 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAIVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHNEKGLYNIHLY
YQEASGTLVGVTGKVTVAGTNSSQEPINENGLPKTGNYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8919

STRAIN M781 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAIVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHNEKGLYNIHLY
YQEASGTLVGVTGKVTVAGTNSSQEPINENGLPKTGNYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8920

STRAIN CJB110 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAIVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHNEKGLYNIHLY
YQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8921

STRAIN 1169NT frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAIVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHNEKGLYNIHLY
YQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8922

STRAIN JM9130013 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFVGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAIVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHNEKGLYNIHLY
YQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVKNEAKISSQTQ

Table 89: Comparative Sequences relating to SAG1350

FTLEKGDKINYDQVLTDGYQWISYKSYSGVRRYIPVKLTTSSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDKVSKQPKVSSPFVEFNFKGKIHVDQVLVDGHQWISYKSYSGIRRYI
EI

PRETTY of: /biotmp/msa255178.2{*} February 11, 2003 08:51 ..

	1				50
msa255178.2{91_090}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_18RS21}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_2603}	mkkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_A909}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_CJB110}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_H36B}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_JM9130013}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_COH1}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_M781}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_M732}	----QVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_1169NT}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
Consensus	*****	*****	*****	*****	*****
	51				100
msa255178.2{91_090}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_18RS21}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_2603}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_A909}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_CJB110}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_H36B}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_JM9130013}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_COH1}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_M781}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_M732}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_1169NT}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
Consensus	*****	*****	*****	*****	*****
	101				150
msa255178.2{91_090}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_18RS21}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_2603}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_A909}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_CJB110}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_H36B}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_JM9130013}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_COH1}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_M781}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_M732}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_1169NT}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
Consensus	*****	*****	*****	*****	*****
	151				200
msa255178.2{91_090}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_18RS21}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_2603}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_A909}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_CJB110}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_H36B}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_JM9130013}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_COH1}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_M781}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_M732}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_1169NT}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
Consensus	*****	*****	*****	*****	*****
	201				250
msa255178.2{91_090}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_18RS21}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_2603}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_A909}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_CJB110}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_H36B}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_JM9130013}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_COH1}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_M781}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_M732}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_1169NT}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
Consensus	*****	*****	*****	*****	*****
	251				300
msa255178.2{91_090}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF
msa255178.2{91_18RS21}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF
msa255178.2{91_2603}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF
msa255178.2{91_A909}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF
msa255178.2{91_CJB110}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF

Table 89: Comparative Sequences relating to SAG1350

msa255178.2{91_H36B}	SFNGVRRFVL	L GKASSVEKT	EDKEKVSQPQ	QARITKTGRL	TIsNETTTGF
msa255178.2{91_JM9130013}	SFNGVRRFVL	L GKASSVEKT	EDKEKVSQPQ	QARITKTGRL	TIsNETTTGF
msa255178.2{91_COH1}	SFNGVRRFVL	L GKASSVEKT	EDKEKVSQPQ	QARITKTGRL	TIsNETTTGF
msa255178.2{91_M781}	SFNGVRRFVL	L GKASSVEKT	EDKEKVSQPQ	QARITKTGRL	TIsNETTTGF
msa255178.2{91_M732}	SFNGVRRFVL	L GKASSVEKT	EDKEKVSQPQ	QARITKTGRL	TIsNETTTGF
msa255178.2{91_1169NT}	SFNGVRRFVL	L GKASSVEKT	EDKEKVSQPQ	QARITKTGRL	TIsNETTTGF
Consensus	*****	*****	*****	*****	*_*-*****
msa255178.2{91_090}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_18RS21}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_2603}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_A909}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_CJB110}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_H36B}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_JM9130013}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_COH1}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_M781}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_M732}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_1169NT}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_18RS21}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_2603}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_A909}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_CJB110}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_H36B}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_JM9130013}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_COH1}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_M781}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_M732}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_1169NT}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTKV	TVAGTNSSQE	PIENGLaKTG
Consensus	*****	*****	*****	*****	*****_***
msa255178.2{91_090}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_18RS21}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_2603}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_A909}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_CJB110}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_H36B}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_JM9130013}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_COH1}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_M781}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_M732}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_1169NT}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	GVRRIIPVKK	L TTSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_18RS21}	GVRRIIPVKK	L TTSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_2603}	GVRRIIPVKK	L TTSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_A909}	GVRRIIPVKK	L TTSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_CJB110}	GVRRIIPVKK	L TTSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_H36B}	GVRRIIPVKK	L TTSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_JM9130013}	GVRRIIPVKK	L TTSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_COH1}	GVRRIIPVKK	L TTSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_M781}	GVRRIIPVKK	L TTSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_M732}	GVRRIIPVKK	L TTSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_1169NT}	GVRRIIPVKK	L TTSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_18RS21}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_2603}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_A909}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_CJB110}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_H36B}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_JM9130013}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_COH1}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_M781}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_M732}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_1169NT}	VSSPVEFNQ	KGEKIHYDQV	LVVDGHWIS	YKSYSGIRRY	IEI
Consensus	*****	*****	*****	*****	***

CLAIMS:

1. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is
5 encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of both GAS and *Streptococcus pneumoniae*.
2. The immunogenic composition of claim 1, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 1.
3. An immunogenic composition comprising a combination of GBS polypeptides, said
10 combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of GAS.
4. The immunogenic composition of claim 3, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 2.
- 15 5. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of *Streptococcus pneumoniae*.
6. The immunogenic composition of claim 5, wherein said GBS polypeptides are encoded
20 by GBS polynucleotide sequences selected from GBS Subset 3.
7. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS serotype polynucleotide sequence which is homologous to at least one other GBS serotype.
- 25 8. The immunogenic composition of claim 2, 4 or 6, wherein one or more of the GBS polypeptides are encoded by GBS serotype polynucleotide sequences which are homologous to at least one other GBS serotype.
9. An immunogenic composition comprising a fusion protein, wherein said fusion protein comprises a first polypeptide sequence which is encoded by a GBS serotype polynucleotide
30 which is conserved across one or more GBS serotypes.
10. A polynucleotide sequence, or a fragment comprising at least 10 contiguous polynucleotides, selected from the sequences set forth on Tables 13 – 31 and 40 – 89.
11. The polynucleotide fragment of claim 10, wherein said fragment is derived from a GBS serotype polynucleotide sequence and is homologous to at least one additional GBS serotype
35 polynucleotide sequence.

Figure 1

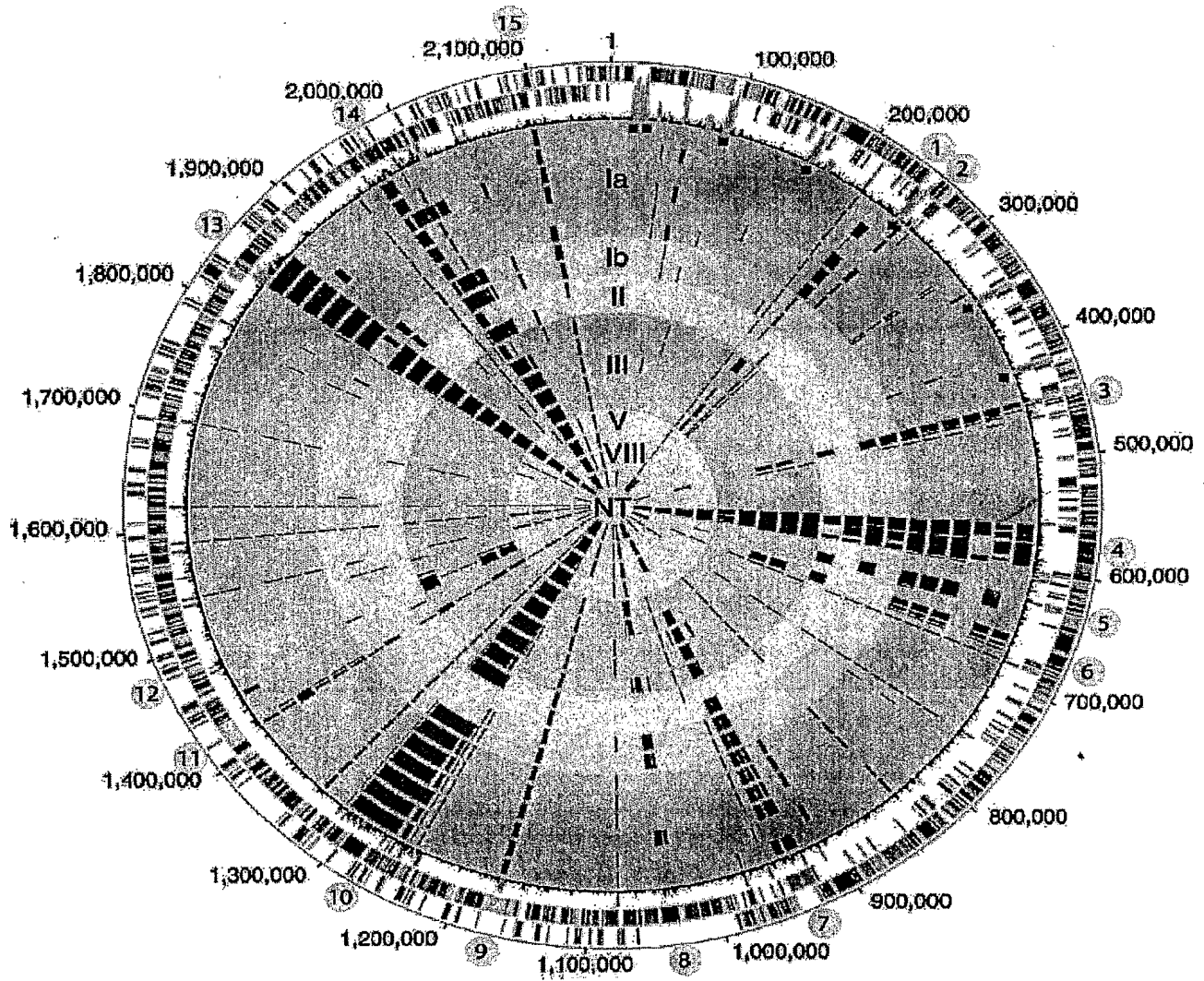


Figure 2

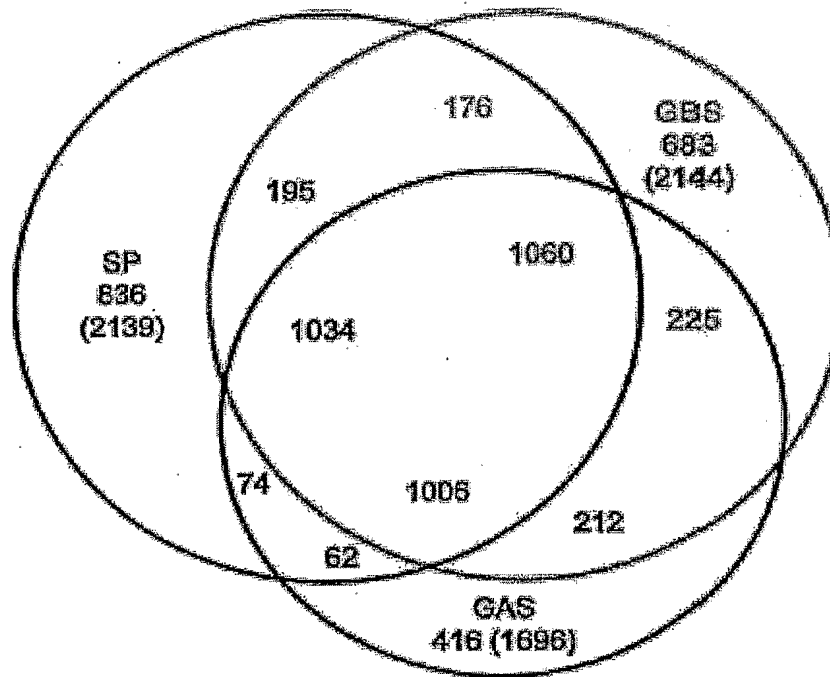
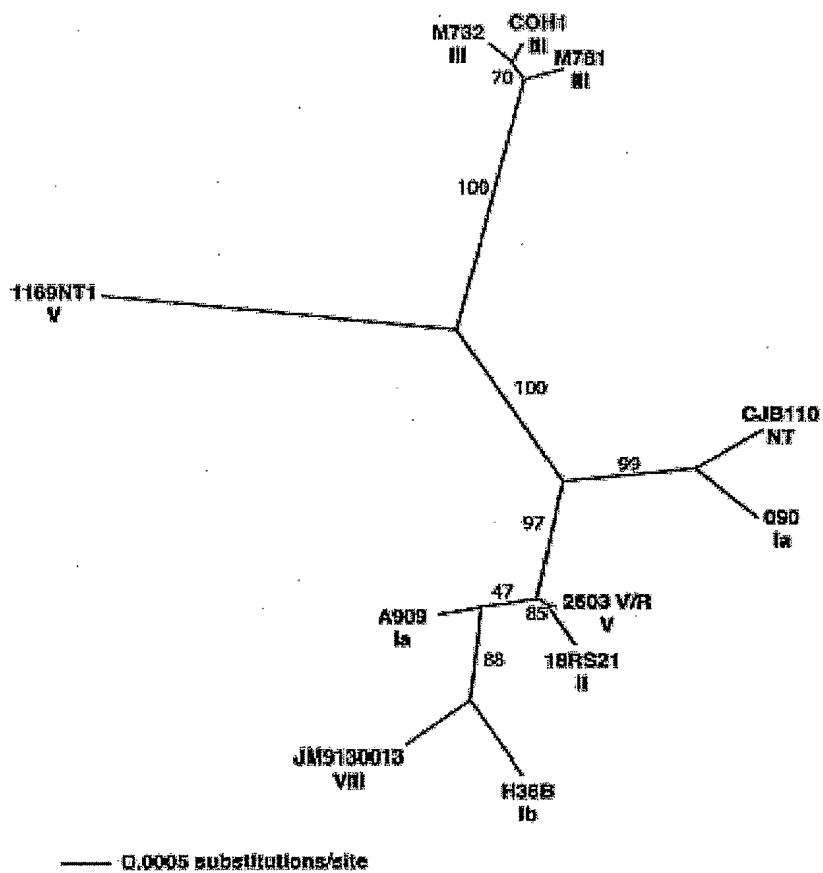


Figure 3



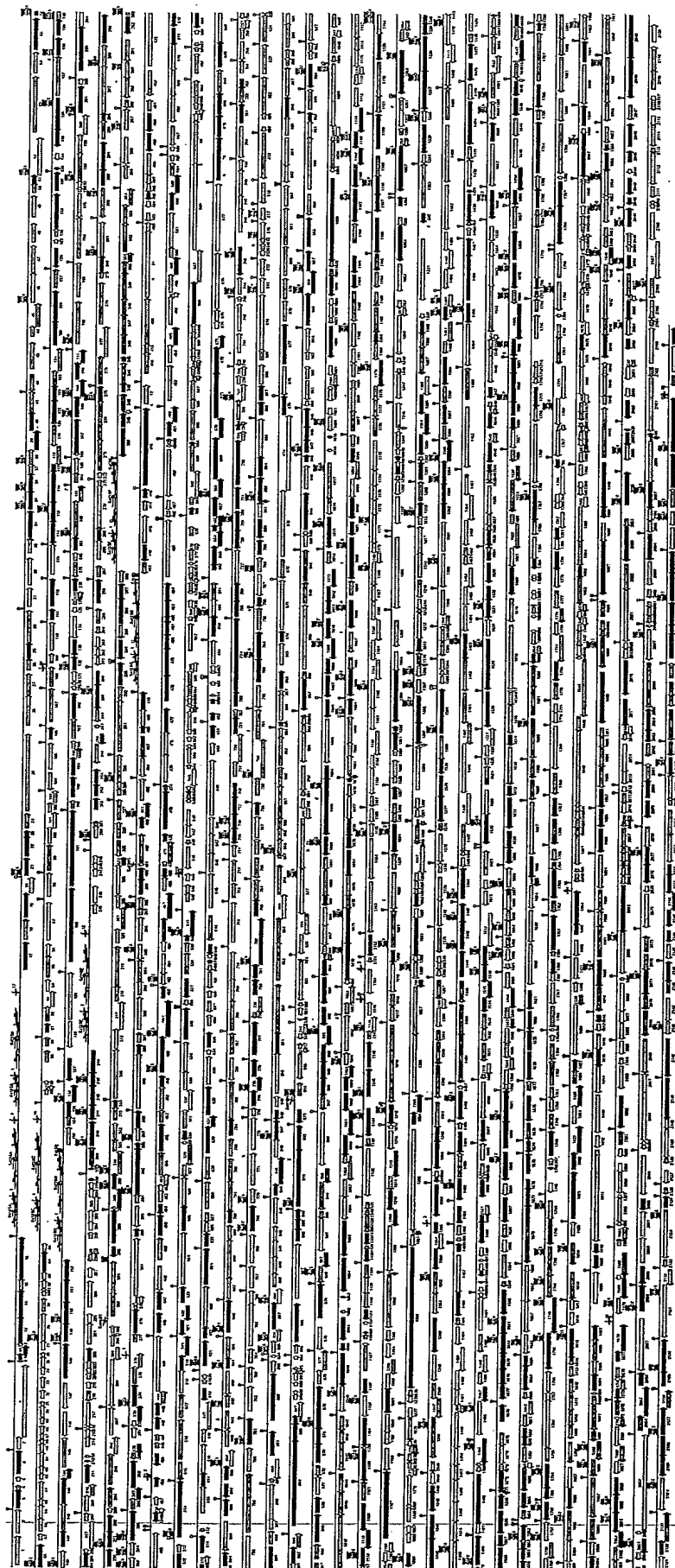


FIGURE 4

